

GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

July 1, 2002, 12:06:52 ; Search time 25.22 Seconds

(without alignments)
68.594 Million cell updates/sec

Title: US-09-147-490-1

Perfect score: 10

Sequence: LVVYPWQRF 10

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Word size : 0

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : SPTRBL_19:*
 1: sp_archea:*
 2: sp_bacteria:*
 3: sp_fungi:*
 4: sp_human:*
 5: sp_invertebrate:*
 6: sp_mammal:*
 7: sp_mhc:*
 8: sp_organelle:*
 9: sp_phage:*
 10: sp_plant:*
 11: sp_rabbit:*
 12: sp_virus:*
 13: sp_vertebrate:*
 14: sp_unclassified:*
 15: sp_rvirus:*
 16: sp_bacteriop:*
 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	100.0	17	4	Q9UMH5	Q9umh5 homo sapien
2	100.0	59	4	Q9BXJ2	Q9bxj2 homo sapien
3	100.0	61	4	Q14842	Q14842 homo sapien
4	100.0	61	4	Q9UBP6	Q9ubp6 homo sapien
5	100.0	61	4	Q14855	Q14855 homo sapien
6	100.0	89	4	Q9PB81	Q9pb81 homo sapien
7	100.0	101	4	Q14477	Q14477 homo sapien
8	100.0	101	4	Q14476	Q14476 homo sapien
9	100.0	105	4	Q9BWU5	Q9bwu5 homo sapien
10	100.0	111	4	Q9BWU6	Q9bwu6 homo sapien
11	100.0	113	4	Q02770	Q02770 callicebus
12	100.0	115	4	Q9ZL19	Q9zl19 homo sapien
13	100.0	123	4	Q14474	Q14474 homo sapien
14	100.0	125	6	Q28221	Q28221 cebus albif
15	100.0	125	6	Q13072	Q13072 callithrix
16	100.0	125	6	Q28799	Q28799 pan troglod

17	100.0	128	4	Q9UK54	Q9uk54 homo sapien
18	100.0	129	4	Q9UL62	Q9ul62 ovis aries
19	100.0	133	6	Q28552	Q28552 periodicus
20	100.0	142	6	Q95233	Q95233 periodicus
21	100.0	142	6	Q13071	Q13071 callithrix
22	100.0	145	6	Q9GY8	Q9gyj8 callicebus
23	100.0	146	6	Q28460	Q28460 mirounga an
24	100.0	147	4	Q9BX96	Q9bx96 homo sapien
25	100.0	147	4	Q96FH7	Q96fh7 homo sapien
26	100.0	147	4	Q96FH6	Q96fh6 homo sapien
27	100.0	147	6	Q9GXK5	Q9gxk5 aotus nancym
28	100.0	147	6	Q28779	Q28779 pan paniscus
29	100.0	147	6	Q88752	Q88752 rattus norvegicus
30	100.0	147	6	Q9GJS7	Q9gjs7 callithrix
31	100.0	155	4	Q14403	Q14403 homo sapien
32	100.0	155	4	Q14473	Q14473 homo sapien
33	100.0	155	6	Q9BRH6	Q9brh6 trichosurus
34	100.0	155	6	Q61650	Q61650 mus musculus
35	100.0	155	6	Q9BEB8	Q9beb8 dasycurus canis
36	100.0	155	4	Q14491	Q14491 homo sapien
37	100.0	155	4	Q9BEB9	Q9beb9 macroscelides proboscideus
38	100.0	155	4	Q9BEB9	Q9beb9 macroscelides proboscideus
39	90.0	155	6	Q9BEB7	Q9beb7 pierametes galloperuviana
40	90.0	155	11	Q9BRZ2	Q9brz2 mus musculus
41	90.0	154	11	Q9WV91	Q9wv91 rattus sp.
42	90.0	154	11	Q9QH8	Q9qh8 dasyurus maculatus
43	90.0	154	11	Q9BEB9	Q9beb9 macroscelides proboscideus
44	90.0	154	11	Q9R056	Q9r056 mus musculus
45	90.0	154	14	Q9BEI7	Q9bei7 macropus eugenii
46	90.0	154	14	Q9BEI1	Q9bei1 sminthopsis
47	90.0	154	14	Q9CYY4	Q9cy4 mus musculus
48	90.0	154	14	Q9CYY2	Q9cy2 mus musculus
49	90.0	154	14	Q9CYY6	Q9cy6 rattus sp.
50	90.0	154	14	Q9CYY8	Q9cy8 mus musculus
51	90.0	154	14	Q9CYY9	Q9cy9 mus musculus
52	90.0	154	14	Q9CYY5	Q9cy5 mus musculus
53	90.0	154	14	Q9CYY12	Q9cy12 mus musculus
54	90.0	154	14	Q9IV86	Q9iv86 m 11 days e
55	90.0	154	14	Q9YGF5	Q9ygf5 oncorhynchus tshawytscha
56	90.0	154	14	Q9BUB9	Q9hub9 noctohenia
57	90.0	154	14	Q9BUB8	Q9hub8 notothenia
58	90.0	154	14	Q9CXZ2	Q9cxz2 mus musculus
59	80.0	154	14	Q90594	Q90594 gallus gallus
60	80.0	154	14	Q9BEB7	Q9beb7 monodelphis domestica
61	80.0	154	14	Q9WQ6	Q9wq6 cricetus
62	80.0	154	14	Q94372	Q94372 peromyscus
63	80.0	154	14	Q92586	Q92586 peromyscus
64	80.0	154	14	Q99MQ7	Q99mq7 cricetus
65	80.0	106	6	Q9XT23	Q9xt23 ceratotherium simum
66	80.0	106	6	Q9XH22	Q9xt22 tapirus terrestris
67	80.0	106	6	Q95183	Q95183 equus caballus
68	80.0	125	11	Q9ZG22	Q9zg22 mus musculus
69	80.0	135	11	Q9D066	Q9d066 rattus norvegicus
70	80.0	140	11	Q61606	Q61606 mus musculus
71	80.0	146	13	P83133	P83133 dipsochelys gigantea
72	80.0	147	11	Q9CZK5	Q9czk5 mus musculus
73	80.0	147	11	Q88753	Q88753 rattus norvegicus
74	80.0	147	11	Q88754	Q88754 rattus norvegicus
75	80.0	147	11	Q9B0677	Q9b0677 rattus norvegicus
76	80.0	147	13	Q90864	Q90864 gallus gallus
77	80.0	147	13	Q90938	Q90938 gallus gallus
78	70.0	147	13	Q95408	Q95408 hominidae
79	70.0	69	13	Q9PWH7	Q9pwh7 morone saxatilis
80	70.0	69	13	Q9PWH5	Q9pwh5 morone saxatilis
81	70.0	105	13	Q90488	Q90488 brachydanio
82	70.0	146	11	Q63011	Q63011 rattus norvegicus
83	70.0	147	11	Q9DB22	Q9db22 mus musculus
84	70.0	147	11	Q9CR49	Q9cr49 mus musculus
85	70.0	147	11	Q92669	Q92669 rattus norvegicus
86	70.0	147	11	Q92670	Q92670 rattus norvegicus
87	70.0	147	13	Q91470	Q91470 salmo salar
88	70.0	147	13	Q9YF4	Q9yf4 oncorhynchus
89	70.0	147	13	Q9PV18	Q9pv18 oncorhynchus

90 7 70.0 147 13 093548
91 7 70.0 147 13 091AJ9
92 7 70.0 147 13 091471
93 7 70.0 147 13 091129
94 7 70.0 147 13 090ZM4
95 7 70.0 148 13 P70073
96 7 70.0 148 13 013140
97 7 70.0 148 13 098851
98 7 70.0 148 13 098852
99 7 70.0 148 13 098853
100 7 70.0 148 13 090485

ALIGNMENTS

093548 brachydanio
091AJ9 notothenia
091471 salmo salar
091129 notothenia
Q90ZM4 epinephelus
P70073 cyprinus ca
013140 cyprinus ca
098851 cyprinus ca
098852 cyprinus ca
098853 cyprinus ca
090485 brachydanio

DR Inter-Pro; IPRO00971; Globin.
DR Pfam; PF00042; globin_1.
DR PRINTS; PR0814; BEPAHAE.M.
DR PROSITE; PS01033; GLOBIN_1.
KW ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 59 59
SQ SEQUENCE 59 AA: 6463 MW: 128EF2C12A13A9D3 CRC64;

Query Match

Best Local Similarity 100.0%; Score 10; DB 4; Length 59;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10
||| | | | | |
Db 33 LVVYPTQRF 42

ALIGNMENTS

RESULT 1

O9UM85

PRELIMINARY;

PRT;

17 AA.

AC O9UM85;

DT 01-MAY-2000 (TREMBREL_13, Created)

DT 01-MAY-2000 (TREMBREL_13, Last sequence update)

DE BETA-GLOBIN PROTEIN (FRAGMENT).

GN BETA-GLOBIN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

SEQUENCE FROM N.A.

RX MEDLINE=6352914; PubMed=8716696;

RA Rahbar S., Nozari G., Forrest G., Gelbart T., Forman S.J., Beutler E.;

RT "A novel intrachromosomal rearrangement in the beta-globin gene found

RL in an African-American family.";

EMBL: S82167; AAC1420.1; -.

HSSP: P02023; 1ABW.

NON_TER 1 1

FT SEQUENCE 17 AA; 2104 MW; 41977E5BE5260504 CRC64;

RP

SEQUENCE FROM N.A.

RN [1]

RP

SEQUENCE FROM N.A.

RX MEDLINE=87299720; PubMed=3620470;

RA Liu J.Z., Harano T., Lanclos K.D., Huisman T.H.;

RT "The beta-delta crossover leading to the beta-delta hybrid gene of

RT hemoglobin P-Nilotic is located within 54 base-pairs of the 5' end of

RT exon 2 or between codons 31 and 50.";

RL Biochim. Biophys. Acta 909:208-212(1987).

RN [2]

RP

SEQUENCE FROM N.A.

RA Fullerton S.M., Bond J.J., Schneider J.A., Hamilton B., Harding R.M.,

RA Boyce A.J., Clegg J.B.;

RT "Polymorphism and divergence in the beta-globin replication origin

RT initiation region." Mol. Biol. Evol. 0:0-0(1999).

CC -1 SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR EMBL: M25660; AAA5313.1; -.

DR EMBL: AF186620; AAC08272.1; -.

DR EMBL: AF186606; AAC08258.1; -.

DR EMBL: AF186608; AAC08260.1; -.

DR EMBL: AF186609; AAC08261.1; -.

DR EMBL: AF186610; AAC08262.1; -.

DR EMBL: AF186611; AAC08263.1; -.

DR EMBL: AF186612; AAC08264.1; -.

DR EMBL: AF186613; AAC08265.1; -.

DR EMBL: AF186615; AAC08267.1; -.

DR EMBL: AF186616; AAC08268.1; -.

DR EMBL: AF186617; AAC08269.1; -.

DR EMBL: AF186618; AAC08270.1; -.

DR EMBL: AF186619; AAC08271.1; -.

DR HSSP: P02023; 1DXT;

DR InterPro; IPRO00971; Globin.

DR Pfam; PF00042; globin_1.

DR PROSITE; PS01033; GLOBIN_1.

DR Fasta; PS01033; GLOBIN_1.

DR KW Heme; Oxygen transport; Respiratory protein.

FT

NON_TER 61 61

SQ SEQUENCE 61 AA: 6691 MW: 905E928EF2C12A13 CRC64;

Query Match

Best Local Similarity 100.0%; Score 10; DB 4; Length 61;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 10; DB 4; Length 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

O9BXA2 PRELIMINARY; PRT; 59 AA.
ID O9BXA2; PRELIMINARY; PRT; 59 AA.
AC O9BXA2; PRELIMINARY; PRT; 59 AA.
DT 01-JUN-2001 (TREMBREL_17, Created)
DT 01-JUN-2001 (TREMBREL_17, Last sequence update)
DT 01-DEC-2001 (TREMBREL_19, Last annotation update)
DE BETA-GLOBIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
DB 2 LVVYPTQRF 11

Query Match 100.0%; Score 10; DB 4; Length 17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

O1484 PRELIMINARY; PRT; 61 AA.
ID O1484; PRELIMINARY; PRT; 61 AA.
AC O14434; PRELIMINARY; PRT; 61 AA.
DT 01-Nov-1996 (TREMBREL_01, Created)
DT 01-Nov-1996 (TREMBREL_01, Last sequence update)
DT 01-COT-2001 (TREMBREL_18, Last annotation update)
DE BETA-HEMOGLOBIN (FRAGMENT).
GN HBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=6352914; PubMed=8716696;

RP SEQUENCE FROM N.A.
RX MEDLINE=87299720; PubMed=3620470;
RA Liu J.Z., Harano T., Lanclos K.D., Huisman T.H.;
RT "The beta-delta crossover leading to the beta-delta hybrid gene of
RT hemoglobin P-Nilotic is located within 54 base-pairs of the 5' end of
RT exon 2 or between codons 31 and 50.";
RL Biochim. Biophys. Acta 909:208-212(1987).

RP SEQUENCE FROM N.A.
RA Fullerton S.M., Bond J.J., Schneider J.A., Hamilton B., Harding R.M.,
RA Boyce A.J., Clegg J.B.;
RT "Polymorphism and divergence in the beta-globin replication origin
RT initiation region." Mol. Biol. Evol. 0:0-0(1999).

CC -1 SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: M25660; AAA5313.1; -.
DR EMBL: AF186620; AAC08272.1; -.
DR EMBL: AF186606; AAC08258.1; -.
DR EMBL: AF186608; AAC08260.1; -.
DR EMBL: AF186609; AAC08261.1; -.
DR EMBL: AF186610; AAC08262.1; -.
DR EMBL: AF186611; AAC08263.1; -.
DR EMBL: AF186612; AAC08264.1; -.
DR EMBL: AF186613; AAC08265.1; -.
DR EMBL: AF186615; AAC08267.1; -.
DR EMBL: AF186616; AAC08268.1; -.
DR EMBL: AF186617; AAC08269.1; -.
DR EMBL: AF186618; AAC08270.1; -.
DR EMBL: AF186619; AAC08271.1; -.
DR HSSP: P02023; 1DXT;
DR InterPro; IPRO00971; Globin.
DR Pfam; PF00042; globin_1.
DR PROSITE; PS01033; GLOBIN_1.

DR Fasta; PS01033; GLOBIN_1.
DR KW Heme; Oxygen transport; Respiratory protein.
FT
SQ SEQUENCE 61 AA: 6691 MW: 905E928EF2C12A13 CRC64;

Query Match 100.0%; Score 10; DB 4; Length 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4

O1484 PRELIMINARY; PRT; 61 AA.
ID O1484; PRELIMINARY; PRT; 61 AA.
AC O14434; PRELIMINARY; PRT; 61 AA.
DT 01-Nov-1996 (TREMBREL_01, Created)
DT 01-Nov-1996 (TREMBREL_01, Last sequence update)
DT 01-COT-2001 (TREMBREL_18, Last annotation update)
DE BETA-HEMOGLOBIN (FRAGMENT).
GN HBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=6352914; PubMed=8716696;

RP SEQUENCE FROM N.A.
RX MEDLINE=87299720; PubMed=3620470;
RA Liu J.Z., Harano T., Lanclos K.D., Huisman T.H.;
RT "The beta-delta crossover leading to the beta-delta hybrid gene of
RT hemoglobin P-Nilotic is located within 54 base-pairs of the 5' end of
RT exon 2 or between codons 31 and 50.";
RL Biochim. Biophys. Acta 909:208-212(1987).

CC -1 SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: M25660; AAA5313.1; -.
DR EMBL: AF186620; AAC08272.1; -.
DR EMBL: AF186606; AAC08258.1; -.
DR EMBL: AF186608; AAC08260.1; -.
DR EMBL: AF186609; AAC08261.1; -.
DR EMBL: AF186610; AAC08262.1; -.
DR EMBL: AF186611; AAC08263.1; -.
DR EMBL: AF186612; AAC08264.1; -.
DR EMBL: AF186613; AAC08265.1; -.
DR EMBL: AF186615; AAC08267.1; -.
DR EMBL: AF186616; AAC08268.1; -.
DR EMBL: AF186617; AAC08269.1; -.
DR EMBL: AF186618; AAC08270.1; -.
DR EMBL: AF186619; AAC08271.1; -.
DR HSSP: P02023; 1DXT;
DR InterPro; IPRO00971; Globin.
DR Pfam; PF00042; globin_1.
DR PROSITE; PS01033; GLOBIN_1.

DR Fasta; PS01033; GLOBIN_1.
DR KW Heme; Oxygen transport; Respiratory protein.
FT
SQ SEQUENCE 61 AA: 6691 MW: 905E928EF2C12A13 CRC64;

QY 1 LVVYPWTQRF 10
 |||||||
 ID Q9UBV6 PRELIMINARY; PRT; 61 AA.
 AC Q9UBV6; 42
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA-GLOBIN (FRAGMENT).
 GN HBB.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA FULLERTON S.M., Bond J., Schneider J.A., Hamilton B., Harding R.M.,
 Boyce A.J., Clegg J.B.;
 "Polymorphism and divergence in the beta-globin replication origin
 initiation region.";
 Mol. Biol. Evol. 0:0-0(1999);
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; AFB86614; AAF02661_1; -;
 DR PR0081; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 61 AA;
 SEQUENCE 61 AA; 6661 MW; 304D818EF2C13435 CRC34;
 DR InterPro; IPR02337; Beta_haem.
 DR Intervro; IPR000971; Globin.
 DR Pfam; PF0004; globin; 1.
 DR PRINTS; PR0081; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 61 AA;
 SEQUENCE 61 AA; 6661 MW; 304D818EF2C13435 CRC34;

Query Match 100.0%; Score 10; DB 4; Length 61;
 Best Local Similarity 100.0%; Pred. No. 3.3e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||||
 ID 33 LVVYPWTQRF 42
 DB

RESULT 5
 014485 PRELIMINARY; PRT; 61 AA.
 ID 014485
 AC 014485; 42
 DT 01-NOV-1995 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE DELTA-HEMOGLBIN (FRAGMENT).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=87299720; PubMed=3620470;
 RA Liu J.Z., Harano T., Lancios K.D., Huisman T.H.;
 "The beta-delta crossover leading to the beta delta hybrid gene of
 hemoglobin P-Niötic is located within 54 base-pairs of the 5' end of
 exon 2 or between codons 31 and 50.";
 RL Biochim. Biophys. Acta 909:208-212(1987).
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; M25601; AAA53154.1; -;
 HSSP; P0203; IDXT
 DR InterPro; IPR000971; Globin.

Query Match 100.0%; Score 10; DB 4; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||||
 ID 33 LVVYPWTQRF 42
 DB

RESULT 7
 014477 PRELIMINARY; PRT; 101 AA.
 ID 014477
 AC 014477; 42
 DT 01-NOV-1995 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HBB PROTEIN (FRAGMENT).
 GN HBB.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

DR Pfam; PF00042; globin; 1.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Respiratory protein.
 FRT NON_TER 61 AA;
 SQ SEQUENCE 61 AA; 6661 MW; D5DC412CC2CDF822 CRC64;

Query Match 100.0%; Score 10; DB 4; Length 61;
 Best Local Similarity 100.0%; Pred. No. 3.3e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||||
 ID 33 LVVYPWTQRF 42
 DB

	RESULT	9
RT	"A fusion gene in man; DNA sequence analysis of the abnormal globin gene of hemoglobin Miyada";	Kimura A., Ohta Y., Fukumaki T., Takegi Y.;
RT	Biochem. Biophys. Res. Commun. 119:968-974(1984).	
RL	-1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.	
CC		
EMBL	K01899; AAAX52635.1; -.	
DR	HSSP; P02023; 1DXT	
DR	InterPro; IPR003337; Beta_haem.	
DR	InterPro; IPR000971; Globin.	
DR	InterPro; IPR002335; Myoglobin.	
DR	PRINTS; PRO0814; BETAHAE.	
DR	PROSITE; PS01033; GLOBIN.	
DR	Erythrocyte; Heme; Oxygen transport; Respiratory protein.	
FT	SEQUENCE 101 AA; 10928 MW; F54FBDB224B5DB0F CRC64;	
SQ		
Query Match	100.0%; Score 10; DB 4; Length 101;	
Best Local Similarity	100.0%; Pred. No. 5e-05;	
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 LVVVPTWTFR 10 42	
RESULT	8	
ID	Q14476 PRELIMINARY; PRT; 101 AA.	
AC	Q14476; 014476; 01-Nov-1995 (TREMBLrel. 01, Created)	
DT	01-Nov-1995 (TREMBLrel. 01, Last sequence update)	
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE	G-GAMMA-HEMOGLOBIN GENE FROM GREEK HPPH MUTANT (FRAGMENT).	
OS	Homo sapiens (Human);	
OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Cetartiodactyla; Homidae; Homo.	
NCBI_TAXID=9606;	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=86017015; PubMed=2413469;	
RA	Stamatoyannopoulos G.; Gelinas R., Yagi M., Endlich B., Lotshaw C., Kazazian H.H.JR. ,	
RT	"Sequences of G-gamma, A-gamma, and beta genes of the Greek (A-gamma) HPPH mutant: evidence for a distal CCAAT box mutation in the A-gamma gene";	
RT	Prog. Clin. Biol. Res. 191:125-139(1985).	
RT	-1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.	
EMBL	M32723; AAA35555.1; -.	
DR	HSPP; P02096; 1FDH.	
DR	InterPro; IPR002337; Beta_haem.	
DR	InterPro; IPR000971; Globin.	
DR	InterPro; IPR02335; Myoglobin.	
DR	PF00042; globin_1.	
DR	PRINTS; PRO0814; BETAHAE.	
DR	PRINTS; PRO0613; MYOGLOBIN.	
DR	PROSITE; PS01033; GLOBIN_1.	
KW	Erythrocyte; Heme; Oxygen transport; Respiratory protein.	
FT	NON_TER 101 101	
SQ	SEQUENCE 101 AA; 11039 MW; 8489025BBDE29BA5 CRC64;	
Query Match	100.0%; Score 10; DB 4; Length 101;	
Best Local Similarity	100.0%; Pred. No. 5e-05;	
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 LVVVPTWTFR 10 42	
RESULT	10	
ID	Q9BW66 PRELIMINARY; PRT; 111 AA.	
AC	Q9BW66; 01-Jun-2001 (TREMBLrel. 17, Created)	
DT	01-Jun-2001 (TREMBLrel. 17, last sequence update)	
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)	
DE	MUTANT_BETA_GLOBIN.	
GN	HBB.	
OS	Homo sapiens (Human);	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Cetartiodactyla; Homidae; Homo.	
NCBI_TAXID=9606;	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=BLOOD;	
RA	Kutlar F., Adekunle A.-D., Leithner C., Kutlar A.;	
RT	"Double heterozygous beta thalassemia mutation (Promoter region - 28 A to C; IVS-II-1 region G to A) was found in a Kuwaiti patient.;"	
RT	Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.	
RL	-1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.	
EMBL	AV027509; AAAX20080.1; -.	
DR	HSSP; P02023; 1DXT	
DR	InterPro; IPR002337; Beta_haem.	
DR	InterPro; IPR000971; Globin.	
DR	PF00042; globin_1.	
DR	PRINTS; PRO0814; BETAHAE.	

DR PROSITE; PS01033; GLOBIN; 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT VARIANT 106 M -> V.
 SQ SEQUENCE 111 AA; 12234 MW; 8992F924B5B3903A CRC64;

Query Match 100.0%; Score 10; DB 4; Length 111;
 Best Local Similarity 100.0%; Pred. No. 5.5e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 Db 33 LVVYPWTQRF 42

RESULT 11
 002770 PRELIMINARY; PRT; 113 AA.
 ID 002770 PRT; 113 AA.
 AC 002770; PRELIMINARY; PRT; 113 AA.
 DT 01-JUL-1997 (TREMBREL. 04, Created)
 RT 01-JUL-1997 (TREMBREL. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBREL. 19, Last annotation update)
 DE EPSILON_GLOBIN (FRAGMENT).
 OS Callitrix argentea (Black-tailed marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
 OX NCBI_TAXID=9482;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9812128; PubMed=9461380;
 RA Porter C.A., Czelusniak J., Schneider H., Sampaio I.,
 RA Goodman M.;
 RT "Sequences of the primate epsilon-globin gene: implications for
 systematics of the marmosets and other New World primates.",
 RL Gene 205:59-71(1997).
 CC -- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; U97025; AAC39571.1; -.
 DR HSSP; P02100; IASW.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000571; Globin.
 DR InterPro; IPR002335; Myoglobin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PR00814; BETAHBEM.
 DR PROSITE; PS00613; MYOGLOBIN.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 113 AA; 12499 MW; 994B77D3BEC81D9D CRC64;

Query Match 100.0%; Score 10; DB 6; Length 113;
 Best Local Similarity 100.0%; Pred. No. 5.5e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 Db 33 LVVYPWTQRF 42

RESULT 12
 09GZL9 PRELIMINARY; PRT; 115 AA.
 ID 09GZL9 PRT; 115 AA.
 AC 09GZL9; PRELIMINARY; PRT; 115 AA.
 DT 01-MAR-2001 (TREMBREL. 16, Created)
 DT 01-MAR-2001 (TREMBREL. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBREL. 19, Last annotation update)
 DE BETA-GLOBIN (MUTANT BETA-GLOBIN) (FRAGMENT).
 GN HBB.
 OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]

RESULT 13
 014474 PRELIMINARY; PRT; 123 AA.
 ID 014474 PRELIMINARY; PRT; 123 AA.
 AC 014474;
 DT 01-NOV-1996 (TREMBREL. 01, Created)
 DT 01-NOV-1996 (TREMBREL. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBREL. 19, Last annotation update)
 DE A-GAMMA-HEMOGLOBIN GENE FROM GREEK HEPH MUTANT (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96017015; PubMed=2413469;
 RA Geimnas R., Yagi M., Endlich B., Lotshaw C., Kazazian H.H.JR. ,
 RA Stamatoyannopoulos G.;
 RT "Sequences of G-gamma, A-gamma, and beta genes of the Greek (A-gamma) HEPH mutant: evidence for a distal CCAAT box mutation in the A-gamma gene.",
 RT Rel. Prog. Clin. Biol. Res. 191:125-139(1995).
 RT -- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; M22724; AAA35953.1; -.
 DR HSSP; P02096; IFDH.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR InterPro; IPR002335; Myoglobin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PR00814; BETAHBEM.
 DR PROSITE; PS00613; MYOGLOBIN.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 123 AA; 123 MW; 7C42739B2FA2FC1 CRC64;

Query Match 100.0%; Score 10; DB 4; Length 123;
 Best Local Similarity 100.0%; Pred. No. 5.9e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 Db 33 LVVYPWTQRF 42

RESULT 14

028221 PRELIMINARY; PRT; 125 AA.
 ID 028221;
 AC 028221;
 DT 01-NOV-1996 (TREMBREL. 01, Created)
 DT 01-NOV-1996 (TREMBREL. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBREL. 19, Last annotation update)
 DE GAMMA-1 GLOBIN.
 GN GAMMA1-GLOBIN.
 OS Cebus albifrons (White-fronted capuchin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Platyrhini; Cebidae; Cebinae; Cebus.
 NCBI_TAXID=9514;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94102157; PubMed=8276414;
 RA Hayasaka K., Skinner C.G., Goodman M., Slightom J.L.;
 RT "The gamma-globin genes and their flanking sequences in primates: findings with nucleotide sequences of capuchin monkey and tarsier.",
 Genomics 18:20-28(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=941115656; PubMed=1342932;
 RA Bailey W.J., Hayasaka K., Skinner C.G., Kehoe S., Sieu L.C.,
 Slightom J.L., Goodman M.;
 RT "Reexamination of the African hominoid trichotomy with additional sequences from the primate beta-globin gene cluster.",
 Mol. Phylogenet. Evol. 1:97-135(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Hayasaka K., Skinner C.G., Slightom J.L., Goodman M.;
 RT "Molecular phylogeny of three platyrhine primates, capuchin monkey, spider monkey, and owl monkey, as inferred from nucleotide sequences of the pseudo-eta-globin gene.",
 RT Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
 -I SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 CC EMBL: M81409; AA19703.1; -.
 DR HSSP; P02096; 1FBH.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 125 AA; ADIC8A3D4919BF CRC64;

Query Match 100.0%; Score 10; DB 6; Length 125;
 Best Local Similarity 100.0%; Pred. No. 6e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Missmatches 0;

Matches 10; Conservative 0; Missmatches 0;

RESULT 16
 ID 028799 PRELIMINARY; PRT; 125 AA.
 AC 028799;
 DT 01-NOV-1996 (TREMBREL. 01, Created)
 DT 01-DEC-2001 (TREMBREL. 19, Last sequence update)
 DE Beta-GLOBIN (FRAGMENT)
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 NCBI_TAXID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8521086; PubMed=3999143;
 RA Savéria P., Trabuchet G., Faure C., Chebloune Y., Gouy M.,
 Verdier G., Nigon V.M.;
 RT "High Rate of Variation in CpG Dinucleotides and in Short Repeated Sequences between Man and Chimpanzee.",
 J. Mol. Biol. 182:21-29(1985).
 CC -I SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: X02345; CAA26204.1; -.
 DR HSSP; P02022; 1DX7.
 DR InterPro; IPR002337; Beta_haem.
 DR Pfam; PF00042; globin_1.
 DR PRINS; PR00814; BEPAHAE.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 125 AA; 13662 MW; 6790E535FF7A11230 CRC64;
 SQ SEQUENCE 125 AA; 13662 MW; 6790E535FF7A11230 CRC64;

Query Match 100.0%; Score 10; DB 6; Length 125;
 Best Local Similarity 100.0%; Pred. No. 6e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Missmatches 0;

Matches 10; Conservative 0; Missmatches 0;

RESULT 17
 ID Q9UK54 PRELIMINARY; PRT; 128 AA.
 AC Q9UK54;
 DT 01-NAY-2000 (TREMBREL. 13, Created)
 DT 01-MAY-2000 (TREMBREL. 13, Last sequence update)
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88121278; PubMed=9461380;
 RA Porter C.A., Czelusniak J., Schneider H., Sampalo I.,
 RA Goodman M.;
 RT "Sequences of the primate epsilon-globin gene: implications for systematics of the marmosets and other New World primates.",
 Gene 205:59-71(1997).

DE HEMOGLOBIN BETA SUBUNIT VARIANT (FRAGMENT).
 GN HBB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 MA Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RA Kutlar F., Holley L., Leithner C., Brisco J., Kutlar A.;
 RT "A silent, very unstable, thalassemic hemoglobin variant, detected by
 RT cDNA sequencing of beta globin mRNA (hemoglobin IIadec Králové) found
 RT in an African American baby.";
 RL Submitted (Aug-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AF181832; ASN00488.1; -.
 DR HSSP: P02023; 1BAB.
 DR InterPro: IPR002337; Beta_hem.
 DR InterPro: IPR000911; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin_1.
 DR PRINTS: PR00814; BEPAHAE.
 DR PRIMUS; PR00613; MYOGLOBIN.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT VARIANT 97 97 D -> A.
 RN NON_TER 1 1
 SQ SEQUENCE 128 AA; 13964 MW; 398B88E71EBE48A2 CRC64;

Query Match 100.0%; Score 10; DB 4; Length 129;
 Best Local Similarity 100.0%; Pred. No. 6.2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 DB 15 LVVYPWTQRF 24

RESULT 19
 ID Q28552 PRELIMINARY; PRT; 133 AA.
 AC Q28552;
 DT 01-NOV-1996 (TREMBLrel. 01, created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE FETAL_GLOBIN
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TAXID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94250599; PubMed=8193169;
 RA Saban J., King D.;
 RT "Sequence of the sheep fetal beta globin gene and flanking region."
 RL Biochim. Biophys. Acta 1218:87-90(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81117280; PubMed=6161931;
 RA Krestschmer P.J., Coon H.C., Davis A., Harrison M., Nienhuis A.W.;
 RT "Hemoglobin switching in sheep: Isolation of the fetal gamma-globin
 gene and demonstration that the fetal gamma- and adult beta-A-globin
 genes lie within eight kilobase segment of homologous DNA.";
 RT J. Biol. Chem. 256:1975-1982(1981).
 DR HSSP; P02070; 1HDA.
 DR InterPro: IPR002337; Beta_hem.
 DR Pfam: PF00042; globin_1.
 DR PRINTS: PR00814; BEPAHAE.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 133 AA; 14780 MW; C0E3736E679BFEGC CRC64;

RESULT 18
 ID Q9UNL6 PRELIMINARY; PRT; 129 AA.
 AC Q9UNL6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HEMOGLOBIN GAMMA-LG (FRAGMENT).
 GN HBG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RA Kutlar F., Prchal J.T., Leithner C., Kutlar A.;
 RT "Nucleotide sequence of the human G-gamma globin messenger RNA
 isolated from whole blood.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AF110493; ASN19655.1; -.
 DR HSSP; P02096; 1FDH.
 DR InterPro: IPR002337; Beta_hem.
 DR InterPro: IPRO00971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin_1.
 DR PRINTS; PR00814; BEPAHAE.
 DR PROSITE; PS01033; GLOBIN.
 DR ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 1 1
 SQ SEQUENCE 129 AA; 14093 MW; 605C30EEBA3B0A4 CRC64;

Query Match 100.0%; Score 10; DB 6; Length 133;
 Best Local Similarity 100.0%; Pred. No. 6.3e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 DB 19 LVVYPWTQRF 28

RESULT 20
 ID Q95233 PRELIMINARY; PRT; 142 AA.
 AC Q95233;
 DT 01-FEB-1997 (TREMBLrel. 02, created)
 DT 01-FEB-1997 (TREMBLrel. 02, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE EPSTIN_GLOBIN (FRAGMENT).
 OS Periodicus potto (potto).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Loridae; Periodicticus.
 OX NCBI_TAXID=9472;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Porter C.A., Page S.L., Czelusniak J., Schneider H., Schneider M.P.C.,

RA Sampalo I., Goodman M.;
 RT "Phylogeny and evolution of selected primates as determined by
 sequences of the epsilon-globin locus and 5' flanking regions.";
 RL Int. J. Primatol. 18:261-295(1997).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 EMBL: U64617; ARB60784.1; -.
 DR HSSP: P02100; 1A9W.
 DR InterPro; IPR00237; Beta_haem.
 DR InterPro; IPR00071; Globin.
 DR InterPro; IPR00235; Myoglobin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PRO0814; BETAHAEIM.
 DR PRINTS; PRO0613; MYOGLOBIN.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 142 AA; 15481 MW; 64D14BC6CCA16AB2 CRC64;
 SQ SEQUENCE 142 AA; 15481 MW; 64D14BC6CCA16AB2 CRC64;

RESULT 21
 ID 013071 PRELIMINARY; PRT; 142 AA.
 AC 013071;
 DT 01-JUL-1997 (TREMBREL_04, Created)
 DT 01-JUL-1997 (TREMBREL_04, Last sequence update)
 DE EPSILON_GLOBIN (FRAGMENT).
 OS Callithrix geoffroyi (Geoffroy's marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
 OX NCBI_TAXID:52231;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE#98121278; PubMed=9461379;
 RA Chiu C.H., Schneider H., Slightom J.L., Gumucio D.I., Goodman M.;
 RT "Dynamics of cis-mediated acquisition of simian gamma-globin gene
 patterns.";
 RL GenBank 205:47-57 (1997).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; AF32379; RAG35072.1; -.
 DR HSSP; P02096; 1F0H.
 DR InterPro; IPR00237; Beta_haem.
 DR InterPro; IPR00071; Globin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PRO0814; BETAHAEIM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 142 AA; 15757 MW; FA329002D22C37c8 CRC64;

SQ SEQUENCE 145 AA; 15757 MW; FA329002D22C37c8 CRC64;

RESULT 22
 ID 013071 PRELIMINARY; PRT; 142 AA.
 AC 013071;
 DT 01-DEC-2001 (TREMBREL_16, Created)
 DT 01-DEC-2001 (TREMBREL_16, Last sequence update)
 DE UNKNOWN EMBL; U97029; AAC39572.1; -.
 DR HSSP; P02100; 1A9W.
 DR InterPro; IPR00233; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR InterPro; IPR00233; Myoglobin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PRO0814; BETAHAEIM.
 DR PROSITE; PRO0613; MYOGLOBIN.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 142 AA; 15522 MW; 8A5480BC2F5BCCC4 CRC64;

Query Match 100.0%; Score 10; DB 6; Length 142;
 Best Local Similarity 100.0%; Pred. No. 6; 7e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFQR 10
 ||||| | | | |
 Db 33 LVVYPWTFQR 42

RESULT 23
 ID 028460 PRELIMINARY; PRT; 146 AA.
 AC 028460;
 DT 01-NOV-1996 (TREMBREL_01, Created)
 DT 01-NOV-1996 (TREMBREL_01, Last sequence update)
 DE UNKNOWN EMBL; U97029; AAC39572.1; -.
 DR HSSP; P02100; 1A9W.
 DR InterPro; IPR00233; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PRO0814; BETAHAEIM.
 DR PROSITE; PRO0613; MYOGLOBIN.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 142 AA; 15522 MW; 8A5480BC2F5BCCC4 CRC64;

Query Match 100.0%; Score 10; DB 6; Length 142;
 Best Local Similarity 100.0%; Pred. No. 6; 7e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFQR 10
 ||||| | | | |
 Db 33 LVVYPWTFQR 42

RESULT 22
 ID 028460 PRELIMINARY; PRT; 145 AA.
 AC 028460;
 DT 01-MAR-2001 (TREMBREL_16, Created)
 DT 01-MAR-2001 (TREMBREL_16, Last sequence update)
 DE GAMMA2-GLOBIN.
 DR GAMMA2-GLOBIN.
 DR Callicebus moloch (dusky titi).
 DR Callitrichidae; Chordata; Craniata; Vertebrata; Euteleostomi;
 DR Mammalia; Eutheria; Primates; Platyrhini; Cebidae; Callicebiniae;
 DR Callitrichidae.
 DR NCB_ Taxid=9523;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE#98121277; PubMed=9461379;
 RA Chiu C.H., Schneider H., Slightom J.L., Gumucio D.I., Goodman M.;
 RT "Dynamics of cis-mediated acquisition of simian gamma-globin gene
 clusters: cis-mediated acquisition of simian gamma-globin gene
 patterns.";
 RL GenBank 205:47-57 (1997).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; AF32379; RAG35072.1; -.
 DR HSSP; P02096; 1F0H.
 DR InterPro; IPR00237; Beta_haem.
 DR InterPro; IPR00071; Globin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PRO0814; BETAHAEIM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 146 AA; 16044 MW; 2543427BF15A711A CRC64;

SQ SEQUENCE 146 AA; 16044 MW; 2543427BF15A711A CRC64;

Query Match 100.0%; Score 10; DB 6; Length 146;
 Best Local Similarity 100.0%; Pred. No. 6.8e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||||
 Db 32 LVVYPWTQRF 41

RESULT 24

QB8X96 PRELIMINARY; PRM; 147 AA.

ID QB8X96
 AC QB8X96:
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE BETA GLOBIN CHAIN VARIANT.
 GN HBB.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE-BLOOD;
 RA Kutlar F., Holley L., Leithner C., Kutlar A.;
 RT "A rare beta chain variant, "Hemoglobin Ty Gard" Pro 124 Glu' found in a
 Caucasian female with erythrocytosis";
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 CC !-- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR EMBL; AF349114; AACN9639.1; -.
 DR HSSP; P02023; IDX7.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR InterPro; IPR002335; Myoglobin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PRO0814; BETAHBM.
 DR PROSITE; PS01033; GLOBIN_1.
 DR KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT VARIANT 125 125 Q->P.
 SEQUENCE 147 AA; 16013 MW; F35A79221C65577A CRC64;

Query Match 100.0%; Score 10; DB 4; Length 147;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||||
 Db 33 LVVYPWTQRF 42

RESULT 25

QB9415 PRELIMINARY; PRM; 147 AA.

ID QB9415
 AC QB9415:
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE EPSTIN-GLOBIN SUBUNIT.

OS Cebus olivaceus (Weeper capuchin), and
 OS Cebus kaapori.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.
 OX NCBI_TaxID:37295; 37294;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=LIMPHOCYTES;
 RX MEDLINE=96111507; PubMed=8845968;
 RA Harada M.L., Schneider H., Schneider M.P., Sampaio I., Czelusniak J.,
 RA Goodman M.;
 RT "DNA evidence on the phylogenetic systematics of New World monkeys":
 RT support for the sister-grouping of Cebus and Saimiri from two unlinked
 RT nuclear genes;"
 RL Phylogenet.; Evol. 4:331-349(1995).
 CC !-- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; U18610; AABA0982.1; -.
 DR U18608; AABA0981.1; -.
 DR HSSP; P02100; 1AQW
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PRO0814; BETAHBM.

DR	PROSITE: PS01033; GLOBIN; 1.	AC	Q03903;
KW	Erythrocyte; Heme; Oxygen transport; Respiratory protein.	DT	01-NOV-1996 (TREMBLrel. 01, Created)
SEQUENCE	147 AA; 16320 MW; 5EFT4B188D314E22 CRC64;	DT	01-NOV-1996 (TREMBLrel. 01, last sequence update)
SQ		DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
QY	1 LVVVPWTQRF 10	DE	HEMOGLOBIN GAMMA-2(N).
Db	33 LVVVPWTQRF 42	OS	Macaca mulatta (Rhesus macaque).
		OC	Bukayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
		OC	Cercopithecinae; Macaca.
		NCBI_TaxID=9544;	
		RN	[1]
		RP	SEQUENCE FROM N.A.
		RX	MEDLINE=91334472; PubMed=1908094;
		RA	Fitch D.H., Bailey W.J., Tagle D.A., Goodman M., Sieu L.,
		RA	Slightron J.L.;
		RA	"Duplication of the gamma-globin gene mediated by 11 long interspersed repetitive elements in an early ancestor of simian primates.";
		RT	Proc. Natl. Acad. Sci. U.S.A. 88:7396-7400(1991).
		RL	[2]
		RP	SEQUENCE FROM N.A.
		RX	MEDLINE=88315036; PubMed=3410846;
		RA	Slightron J.L., Koop B.F., Xu P., Goodman M.;
		RA	"Rhesus fetal globin genes. concerted gene evolution in the descent of higher primates.";
		RT	J. Biol. Chem. 263:12427-12438(1988).
		RL	-- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
		CC	EMBL; M53419; CAL37498.1; -.
		DR	DR
		DR	InterPro: IPR002337; Beta_haem.
		DR	InterPro: IPR000971; Globin.
		DR	Pfam: PF00042; globin_1.
		DR	PRINTS: PR00814; BEPAAEM.
		DR	PROSITE: PS01033; GLOBIN; 1.
		KW	Erythrocyte; Heme; Oxygen transport; Respiratory protein.
		SQ	SEQUENCE 147 AA; 16127 MW; 885444926B997F CRC64;
RESULT	28		
ID	003901 PRELIMINARY; PRT; 147 AA.		
AC	Q03901; 01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DE			
DE			
OS			
OC			
OC			
OC			
NCBI_TaxID=9544;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=91210254; PubMed=2019578;		
RA	Tagle D.A., Slightron J.L., Jones R.T., Goodman M.;		
RT	"Concerted evolution led to high expression of a prosimian primate delta globin gene locus";		
RT	J. Biol. Chem. 266:7469-7480(1991).		
RL	[2]		
RC	SEQUENCE FROM N.A.		
RX	TISSUE=LIVER;		
RA	Tagle D.A., Stahnheide M.J., Siemieniak D.R., Benson P., Goodman M.,		
RA	Slightron J.L.;		
RT	"The beta globin gene cluster of the prosimian primate Galago crassicaudatus: nucleotide sequence determination of the 41-kb cluster and comparative sequence analyses";		
RT	Genomics 13:741-760(1992).		
RL	[3]		
RC	SEQUENCE FROM N.A.		
RP	TISSUE=LIVER;		
RA	Slightron J.L.;		
RL	Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.		
RL	-1-SIMILARITY: BELONGS TO THE GLOBIN FAMILY.		
DR	EMBL; M61740; AAA35445.1; -.		
DR	EMBL; U60902; AAC50963.1; -.		
DR	HSSP; P02023; IDXT.		
DR	InterPro: IPR02337; Beta_haem.		
DR	InterPro: IPR000971; Globin.		
DR	Pfam: PF00042; globin_1.		
DR	PRINTS: PR00814; BEPAAEM.		
DR	PROSITE: PS01033; GLOBIN; 1.		
DR	Erythrocyte; Heme; Oxygen transport; Respiratory protein.		
KW	SEQUENCE 147 AA; 16085 MW; 2AC69B468D0011B5 CRC64;		
QY	1 LVVVPWTQRF 10		
Db	33 LVVVPWTQRF 42		
RESULT	30		
ID	004587 PRELIMINARY; PRT; 147 AA.		
AC	Q0G1S7; 01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	GAMMA1-GLOBIN (GAMMA2-GLOBIN).		
GN	GAMMA1-GLOBIN.		
OS	Calithrix jacchus (Common marmoset).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrhini; Callitrichidae; Callitrix.		
OC			
OC			
NCBI_TaxID=9403;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=9812277; PubMed=9461379;		
RA	Chiu C.H., Schneider H., Slightron J.L., Gumucio D.L., Goodman M.;		
RT	"Dynamics of regulatory evolution in primate beta-globin gene clusters: cis-mediated acquisition of simian gamma fetal expression patterns";		
RT	Gene 205:47-57(1997).		
RL	-- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.		
CC	-		
DR	EMBL; AF016991; AAC35074.1; -.		
DR	HSSP; P02096; 1FDH.		
DR	InterPro: IPR02337; Beta_haem.		
RESULT	29		
ID	003903 PRELIMINARY; PRT; 147 AA.		
QY	1 LVVVPWTQRF 10		
Db	33 LVVVPWTQRF 42		

Query Match 100.0%; Score 10; DB 6; Length 147;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 33 LVVYPWTQRF 42

RESULT 31
 O9GLX7 PRELIMINARY; PRT; 147 AA.
 ID O9GLX7;
 AC O9GLX7;
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 RL 01-MAR-2001 (TREMBLrel. 19, Last annotation update?)
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DE HYBRID GAMMA1/GAMMA2-GLOBIN.
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98121277; PUBMED=9461379;
 RA Chiu C.H., Schneider H., Slightom J.L., Gumucio D.L., Goodman M.;
 RT "Dynamics of regulatory evolution in primate beta-globin gene
 clusters: cis-mediated acquisition of simian gamma fetal expression
 patterns.", "TREMBLrel. 16, Last sequence update")
 RL Gene 205:47-57(1997).
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AF016983; AAG33925.1; -.
 DR HSSP; P02096; IFDH.
 DR InterPro; IPR00971; Globin.
 DR InterPro; IPR002335; Myoglobin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PRO0814; BETHAEM.
 DR PROSITE; PS01033; MYOGLOBIN.
 DR PRINTS; PRO0814; BETHAEM.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR00971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PRO0814; BETHAEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 DR Erythrocyte; Heme; oxygen transport; Respiratory protein.
 KW SEQUENCE 147 AA; 15957 MW; 01F417F8C1582B26 CRC64;

Query Match 100.0%; Score 10; DB 6; Length 147;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 33 LVVYPWTQRF 42

RESULT 33
 O9GLX5 PRELIMINARY; PRT; 147 AA.
 ID O9GLX5;
 AC O9GLX5;
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 RL 01-MAR-2001 (TREMBLrel. 19, Last annotation update)
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DE HYBRID GAMMA1/GAMMA2-GLOBIN.
 OS Aotus nancymaae (Owl monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_TaxID=37293;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98121277; PUBMED=9461379;
 RA Chiu C.H., Schneider H., Slightom J.L., Gumucio D.L., Goodman M.;
 RT "Dynamics of regulatory evolution in primate beta-globin gene
 clusters: cis-mediated acquisition of simian gamma fetal expression
 patterns.", "TREMBLrel. 16, Last sequence update")
 RL Gene 205:47-57(1997).
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AF016985; AAG33927.1; -.
 DR HSSP; P02096; IFDH.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR00971; Globin.
 DR InterPro; IPR002335; Myoglobin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PRO0814; BETHAEM.
 DR PROSITE; PS01033; MYOGLOBIN.
 DR Erythrocyte; Heme; oxygen transport; Respiratory protein.
 KW SEQUENCE 147 AA; 15896 MW; B5F417E994F60FB CRC64;

Query Match 100.0%; Score 10; DB 6; Length 147;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 33 LVVYPWTQRF 42

RESULT 32
 O9GLX6 PRELIMINARY; PRT; 147 AA.
 ID O9GLX6;
 AC O9GLX6;
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 RL 01-MAR-2001 (TREMBLrel. 19, Last annotation update)
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DE HYBRID GAMMA1/GAMMA2-GLOBIN.
 OS Saimiri ustus (Squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.

OX NCBI_TaxID=66265;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98121277; PUBMED=9461379;
 RA Chiu C.H., Schneider H., Slightom J.L., Gumucio D.L., Goodman M.;
 RT "Dynamics of regulatory evolution in primate beta-globin gene
 clusters: cis-mediated acquisition of simian gamma fetal expression
 patterns.", "TREMBLrel. 16, Last sequence update")
 RL Gene 205:47-57(1997).
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AF016984; AAG33926.1; -.
 DR HSSP; P02096; IFDH.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR00971; Globin.
 DR InterPro; IPR002335; Myoglobin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PRO0814; BETHAEM.
 DR PROSITE; PS01033; MYOGLOBIN.
 DR Erythrocyte; Heme; oxygen transport; Respiratory protein.
 KW SEQUENCE 147 AA; 15957 MW; 01F417F8C1582B26 CRC64;

Query Match 100.0%; Score 10; DB 6; Length 147;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 33 LVVYPWTQRF 42

RESULT 34
ID Q28779 PRELIMINARY; PRT; 147 AA.
DT 01-NOV-1996 (TREMBREL_01, Created)
DT 01-NOV-1996 (TREMBREL_01, Last sequence update)
DT 01-DEC-2001 (TREMBREL_19, Last annotation update)
DE DNA.
OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NCBI_TaxID=9597;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9411596; PubMed=1342932;
RA Bailey W.J., Hayasaka K., Skinner C.G., Kehoe S., Sieu L.C.,
RA Slightom J.L., Goodman M.;
RT "Reexamination of the African hominoid trichotomy with additional
sequences from the primate beta-globin gene cluster.";
RL Mol. Phylogenet. Evol. 1:97-135(1992).
CC -i SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: M97116; AAB7113.1; -.
DR HSSP: P02096; IFDH;
DR InterPro: IPR02337; Beta_haem.
DR IntePro: IPR0042; Globin.
DR Pfam: PF00042; globin_1.
DR PRINTS: PR0014; BETAHEM.
DR PROSITE: PS01033; GLOBIN_1.
DR ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
KW SEQUENCE; 147 AA; 16168 MW; 8FCDD1527AC66DDE CRC64;
SQ

Query Match 100.0%; Score 10; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 33 LVVYPWTQRF 42

RESULT 35
ID 088752 PRELIMINARY; PRT; 147 AA.
AC 088752
DT 01-NOV-1998 (TREMBREL_08, Created)
DT 01-NOV-1998 (TREMBREL_08, Last sequence update)
DT 01-DEC-2001 (TREMBREL_19, Last annotation update)
DE EPSTION 1.
GN RATTUS NORVEGICUS.
OS Rattus norvegicus (Rat).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RA HIROYUKI S.;
RL Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RX MEDLINE=9921407; PubMed=10196478;
RA Sato H., Inokuchi N., Nagae Y., Okazaki T.;
RT "Molecular cloning and characterization of two sets of alpha-theta
genes in the rat alpha-like globin gene cluster.";
RL Gene 23(9):91-99(1999).
CC -i SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: X56326; CAM39765.1; -.
DR HSSP: P02100; IAFH;
DR InterPro: IPR02337; Beta_haem.

RESULT 36
ID Q14491 PRELIMINARY; PRT; 152 AA.
AC Q14491;
DT 01-NOV-1996 (TREMBREL_01, Created)
DT 01-NOV-1996 (TREMBREL_01, Last sequence update)
DT 01-DEC-2001 (TREMBREL_19, Last annotation update)
DE HEMOGLOBIN GAMMA-G (FRAGMENT).
GN HBG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NCBI_TaxID=9606;
OX

[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=61237788; PubMed=7250702;
RA Cavalllesco C., Forget B.G., deRiel J.K., Wilson L.B., Wilson J.T.,
RA Weissman S.M.;
RT "Nucleotide sequence of human G gamma globin messenger RNA."
RL Gene 12:215-221(1980).
CC -i SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: M15386; AAB0159.1; -.
DR HSSP: P02096; IFDH;
DR InterPro: IPR02337; Beta_haem.
DR IntePro: IPR00971; Globin.
DR InterPro: IPR02335; Myoglobin.
DR Pfam: PF00042; globin_1.
DR PRINTS: PR00814; BETAHEM.
DR PRINTS: PR00613; MYOGLOBIN.
DR PROSITE: PS01033; GLOBIN_1.
KW ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
FT NON_TER
SEQUENCE 152 AA; 16594 MW; F13FF6666ECE879 CRC64;

Query Match 100.0%; Score 10; DB 4; Length 152;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 38 LVVYPWTQRF 47

RESULT 37
ID 014403 PRELIMINARY; PRT; 155 AA.
AC 014403;
DT 01-NOV-1996 (TREMBREL_01, Created)
DT 01-NOV-1996 (TREMBREL_01, Last sequence update)
DT 01-DEC-2001 (TREMBREL_19, Last annotation update)
DE GAMMA-G GLOBIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;

[1] RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Vladimir V., Kavsan V.M.;
 RL Submitted (SEP-1990) to the EMBL/GenBank/DDBJ databases.
 [2] RN
 SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Dmitrenko V.V., Kavsan V.M.;
 RT Nucleotide sequence of mitochondrial cytochrome c oxydase II from
 human fetal liver.";
 RL Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
 -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 CC EMBL; X55556; CAA39189.1; -. HSSP; P02096; 1FDH.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR InterPro; IPR002335; Myoglobin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PRO0814; BETAHAEM.
 DR PRINTS; PR00613; MYOGLOBIN.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
 FT NON-TER 1 1 155 AA; 16969 MW; FEB0151ABA4B6BF CRC64;
 SQ SEQUENCE 155 AA; 16969 MW; FEB0151ABA4B6BF CRC64;

Query Match 100.0%; Score 10; DB 4; Length 155;
 Best Local Similarity 100.0%; Pred. No. 7.2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTQRF 10
 Db 26 LVVYPWTQRF 35

RESULT 38
 014473 ID PRELIMINARY; PRT; 175 AA.
 AC 014473;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA-GLOBIN GENE FROM A THALASSEMIA PATIENT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoide; Homo.
 RN NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE90251659; PubMed=1971109;
 RA Thein S.L., Hesketh C., Taylor P., Temperley I.J., Hutchinson R.M.,
 RA Old J.M., Wood W.G., Cleeg J.B., Weatherall D.J.;
 RT "Molecular basis for dominantly inherited inclusion body beta-
 thalassemia.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3924-3928(1990).
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; M34059; AAA35525.1; -. EMBL; M34058; AAA35525.1; JOINED.
 DR HSSP; P02023; IDXT Interpro; IPR000971; Globin.
 DR pfam; PF00042; globin; 1.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Respiratory protein.
 SEQUENCE 175 AA; 18931 MW; E87DBB659A3E9950 CRC64;

Query Match 100.0%; Score 10; DB 4; Length 175;
 Best Local Similarity 100.0%; Pred. No. 7.9e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTQRF 10
 Db 33 LVVYPWTQRF 42

RESULT 39
 09BEH6 ID PRELIMINARY; PRT; 52 AA.
 AC 09BEH6;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE OMEGA GLOBIN (FRAGMENT);
 OS Trichosurus vulpecula (Brush-tailed possum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21107677; PubMed=11158601;
 RA Wheeler D., Hope R., Cooper S.J., Dolman G., Webb G.C., Bottema C.D.,
 RA Gooley A.A., Goodman M., Holland R.A.;
 RT "An orphaned mammalian beta-globin gene of ancient evolutionary
 origin";
 RL proc. Natl. Acad. Sci. U.S.A. 98:1101-1106(2001).
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; AV014775; AAC11490.1; -. HSSP; P02118; 1A4F.
 DR InterPro; IPR002337; Beta_haem.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PRO0814; BETAHAEM.
 DR PRINTS; PR00613; GLOBIN; 1.
 DR PROSITE; PS01033; GLOBIN; 1.
 DR InterPro; IPR000971; Globin.
 FT NON-TER 52 52 52 AA; 5736 MW; CD90D1378E59037 CRC64;
 SQ SEQUENCE 52 AA; 5736 MW; CD90D1378E59037 CRC64;

Query Match 90.0%; Score 9; DB 6; Length 52;
 Best Local Similarity 100.0%; Pred. No. 0.0047; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTQRF 9
 Db 13 LVVYPWTQRF 21

RESULT 40
 061650 ID PRELIMINARY; PRT; 52 AA.
 AC 061650;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA-GLOBIN (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80132479; PubMed=7357610;
 RA Pavlakis G.N., Lockard R.E., Vamvakopoulos N., Rieser L.,
 RA RajBhandary U.L., Vourakis J.N.;
 RT "Secondary structure of mouse and rabbit alpha- and beta-globin mRNAs:
 RT differential accessibility of alpha and beta initiator AUG codons
 RT towards nucleoses";
 RL Cell 91:1021-1026(1998).
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; M10524; AAA37705.1; -. HSSP; P02023; IDXT.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PROSITE; PS01033; GLOBIN; 1.

RA	Heme; Oxygen transport; Respiratory protein.
RT	"An orphaned" mammalian beta-globin gene of ancient evolutionary origin.";
RT	Proc. Natl. Acad. Sci. U.S.A. 98:1101-1106(2001).
RL	-- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC	EMBL: AY014772; AAK11487.1; -.
DR	HSSE: P021F1; 1A4F.
DR	InterPro: IPR002337; Beta_haem.
DR	InterPro: IPR000971; Globin.
DR	Pfam: PF00042; globin; 1.
DR	PRINTS: PR00814; BETAHAEM.
DR	PROSITE: PS01033; GLOBIN; 1.
KW	Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT	NON_TER 1
FT	NON_TER 1
SQ	SEQUENCE 58 AA; 6390 MW; 3B4A24F723D2BC2A CRC64;
RESULT	41
Q9BEH8	PRELIMINARY; PRT; 54 AA.
ID	Q9BEH8;
AC	Q9BEH8;
DT	01-JUN-2001 (TREMBREL. 17, Created)
DT	01-JUN-2001 (TREMBREL. 17, Last sequence update)
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)
DE	OMEGA GLOBIN (FRAGMENT).
OS	Dasyurus viverrinus (Southeastern quoll).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Metatheria; Dasyuromorpha; Dasyuridae; Dasyurus.
OX	NCBI_TAXID=9279;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21107677; PubMed=11158601;
RA	Wheeler D., Hope R., Cooper S.J., Dolman G., Webb G.C., Bottema C.D., Gooley A.D., Goodman M., Holland R.A.;
RA	"An orphaned mammalian beta-globin gene of ancient evolutionary origin.;"
RT	Proc. Natl. Acad. Sci. U.S.A. 98:1101-1106(2001).
RL	-1 SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC	EMBL: AY014773; AAK11488.1; -.
DR	HSSE: P02118; 1A4F.
DR	InterPro: IPR002337; Beta_haem.
DR	InterPro: IPR000971; Globin.
DR	Pfam: PF00042; globin; 1.
DR	PRINTS: PR00814; BETAHAEM.
DR	PROSITE: PS01033; GLOBIN; 1.
KW	Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT	NON_TER 1
FT	NON_TER 1
SQ	SEQUENCE 54 AA; 6059 MW; 9D370673B475C499 CRC64;
RESULT	42
Q9BEH9	PRELIMINARY; PRT; 58 AA.
ID	Q9BEH9;
AC	Q9BEH9;
DT	01-JUN-2001 (TREMBREL. 17, Created)
DT	01-JUN-2001 (TREMBREL. 17, Last sequence update)
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)
DE	OMEGA GLOBIN (FRAGMENT).
OS	Macropus giganteus (Eastern gray kangaroo).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX	NCBI_TAXID=9317;
RP	SEQUENCE FROM N.A.
RN	[1]
RR	MEDLINE=21107677; PubMed=11158601;
RA	Wheeler D., Hope R., Cooper S.J., Dolman G., Webb G.C., Bottema C.D.,
RESULT	43
Q9BM3	PRELIMINARY; PRT; 59 AA.
ID	Q9BM3
AC	Q9BM3;
DT	01-JUN-2001 (TREMBREL. 17, Created)
DT	01-JUN-2001 (TREMBREL. 17, Last sequence update)
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)
DE	TRUNCATED_BETA-GLOBIN.
GN	HBB.
OS	Hom sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX	NCBI_TAXID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Yang Z., Chu J., Ban G., Lin K., Shi L., Tao Y., Sun H.; "Molecular characterization of beta thalassemia in Yunnan, China.;" Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RT	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RL	-1 SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC	EMBL: AF31979; AAK28066.1; -.
DR	HSSE: P02023; 1DXT.
DR	InterPro: IPR000971; Globin.
DR	Pfam: PF00042; globin; 1.
DR	PROSITE: PS01033; GLOBIN; 1.
KW	Heme; Oxygen transport; Respiratory protein.
SQ	SEQUENCE 59 AA; 6542 MW; 84936430BD1E09F1 CRC64;
RESULT	44
Q9BEH7	PRELIMINARY; PRT; 60 AA.
ID	Q9BEH7
AC	Q9BEH7;
DT	01-JUN-2001 (TREMBREL. 17, Created)
DT	01-JUN-2001 (TREMBREL. 17, Last sequence update)
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)
DE	OMEGA GLOBIN (FRAGMENT).
OS	Perameles gunnii (Eastern barred bandicoot).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Peramelemorphia; Peramelidae; Perameles.
 NCBL_TAXID=37737;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2110677, PubMed=11159601;
 RA Wheeler D., Hope R., Cooper S.J., Dolman G., Webb G.C., Bottema C.D.,
 RA Gooley A.A., Goodman M., Holland R.A.;
 RT "An orphaned mammalian beta-globin gene of ancient evolutionary
 RT origin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1101-1106(2001).
 CC !- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; AY014774; AAK11489.1; -.
 DR HSSP; P02118; 1A4F.
 DR InterPro; IPR002337; Beta_haem.
 DR Pfam; PF00042; globin_1.
 DR PRINS; PS01033; GLOBIN.
 DR ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.
 FT NON_TER 1
 FT NON_TER 60
 SQ SEQUENCE 60 AA; 6585 MW; 6FA8AFF6123F2CE7 CRC64;

Query Match 90.0%; Score 9; DB 6; Length 60;
 Best Local Similarity 100.0%; Pred. No. 0.00053; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; MisMatches 0;

OY 1 LVVYPWTQR 9
 |||||
 21 LVVYPWTQR 29

RESULT 45

ID 99CRZ2 PRELIMINARY; PRT; 134 AA.

AC 99CRZ2;
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBrel. 17, Last annotation update)
 DE 13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
 DE CLONE:2510040N07, FULL INSERT SEQUENCE (FRAGMENT).

GN HBB-B1.
 OS Mus musculus (mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC LIVER;
 RX MEDLINE=21085660; PubMed=1121851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kiyosawa H., Kondo H., Adachi J., Fukuda I.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,
 RA Saito T., Okazaki Y., Gotoh T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann M., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Schuelke M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blawie J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Montaert P.,
 RA Nordone P., Ring B., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shiba T., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohotsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001);
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

RESULT 46

ID 09QW91 PRELIMINARY; PRT; 146 AA.

AC 09QW91;
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBrel. 13, Last annotation update)
 DR 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE BETA 2 GLOBIN.
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94185903; PubMed=8138033;
 RA Ferranti P., Carbone V., Sannolo N., Fiume I., Malorni A.;
 RT "Mass spectrometric analysis of rat hemoglobin by FAB-overlapping
 RT chains";
 RT Int. J. Biochem. 25:1943-1950(1993).
 RL Int. J. Biochem. 25:1943-1950(1993).
 CC !- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR HSSP; P02023; 1B8B.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR00971; Globin.
 DR InterPro; IPR002335; Myoglobin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PRO0814; BETAHAE.
 DR PRINTS; PRO0613; MYOGLOBIN.
 DR PROSITE; PS01033; GLOBIN.
 DR ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.
 FT NON_TER 1
 SQ SEQUENCE 134 AA; 14394 MW; A92A8CBBE8231F29 CRC64;

Query Match 90.0%; Score 9; DB 11; Length 134;
 Best Local Similarity 100.0%; Pred. No. 0.001; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; MisMatches 0;

OY 1 LVVYPWTQR 9
 |||||
 20 LVVYPWTQR 28

RESULT 47

ID 09QUT6 PRELIMINARY; PRT; 146 AA.

AC 09QUT6;
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBrel. 13, Last annotation update)

DE BEWA 1 GLOBIN.
 OS Rattus sp.;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94185903; PubMed=8138033;
 RA Ferranti P., Carbone V., Sannolo N., Flume I., Malorni A.;
 RT "Mass spectrometric analysis of rat hemoglobin by FAB-overlapping.
 RT chains.";
 RT INT. J. Biochem. 25:1943-1950(1993).
 RT '- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 RL HSP; P02023; IBAK.
 DR InterPro; IPR002337; Beta haem.
 DR InterPro; IPR00971; Globin.
 DR InterPro; IPR002335; Myoglobin.
 DR Pfam; PF00042; globin_1.
 DR Prints; PRO0814; BETAHEM.
 DR PROSITE; PS01033; GLOBIN_1.
 DR ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
 KW SEQUENCE; 146 AA; 15834 MW; 3E04BPF5C875D23 CRC64;
 SQ

RESULT 48

Q9QUN8 PRELIMINARY; PRT; 146 AA.

ID Q9QUN8; PRELIMINARY; PRT; 146 AA.

AC Q9QUN8; PRELIMINARY; PRT; 146 AA.

DT 01-MAY-2000 (TREMBREL_13, Created)

DT 01-MAY-2000 (TREMBREL_13, Last sequence update)

DT 01-DEC-2001 (TREMBREL_19, Last annotation update)

DE BETA-1-GLOBIN (FRAGMENT).

DR HBB; MUS_musculus (Mouse).
 DR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99373250; PubMed=10441738;
 RA Ueda Y., Mirashita N., Imai K., Yamaguchi Y., Takamura K.,
 RA Notohara M., Shiroishi T., Kawashima T., Ning L., Wang C., Wu X.,
 RA Moriwaki K.; sequences of the mouse globin beta gene cDNAs in a wild
 RT derived new haplotype Hbbwl.;
 RL Mamm. Genome 10:879-882(1999).
 RT '- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; AB020013; BAB7353.1; -.
 DR HSSP; P02023; BAB.
 DR MGDB; MGJ_96020; HBB.
 DR InterPro; IPR002337; Beta haem.
 DR InterPro; IPR00971; Globin.
 DR Pfam; PF00042; globin_1.
 DR Prints; PRO0814; BETAHEM.
 DR PROSITE; PS01033; GLOBIN_1.
 DR ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
 KW FT NO_TER
 FT SEQUENCE; 146 AA; 15709 MW; 7C4504CB26D197A5 CRC64;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99373250; PubMed=10441738;
 RA Ueda Y., Miyashita N., Imai K., Yamaguchi Y., Takamura K.,
 RA Notohara M., Shiroishi T., Kawashima T., Ning L., Wang C., Wu X.,
 RA Moriwaki K.;
 RT "Nucleotide sequences of the mouse globin beta gene cDNAs in a wild
 RT derived new haplotype Hbbwl.";
 RL Mamm. Genome 10:879-882(1999).
 CC '- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; AB020014; BAB7354.1; -.
 DR HSSP; P02023; BAB.
 DR MGDB; MGJ_96020; Hbb.
 DR InterPro; IPR002337; Beta haem.
 DR InterPro; IPR00971; Globin.
 DR InterPro; IPR002335; Myoglobin.
 DR Pfam; PF00042; globin_1.
 DR Prints; PRO0814; BETAHEM.
 DR PROSITE; PS01033; GLOBIN_1.
 DR ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
 KW FT NO_TER
 FT SEQUENCE; 146 AA; 15709 MW; 7C4504CB26D197A5 CRC64;

RESULT 50

Q9BR12 PRELIMINARY; PRT; 147 AA.

ID Q9BR12; PRELIMINARY; PRT; 147 AA.

AC Q9BR12; PRELIMINARY; PRT; 147 AA.

DT 01-JUN-2001 (TREMBREL_17, Created)

DT 01-JUN-2001 (TREMBREL_17, Last sequence update)

DT 01-DEC-2001 (TREMBREL_19, Last annotation update)

DE OMSCA_GLOBIN.

OS Macropus_eugenii (Tamar wallaby).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxID=9315;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21107677; PubMed=11158601;
 RA Wheeler D., Hope R., Cooper S.J., Dolman G., Webb G.C., Bottema C.D.,

RA	Gooley A.A., Goodman M., Holland R.A.;	AC	Q9CY54;
RT	"An orphaned mammalian beta-globin gene of ancient evolutionary origin.";	RT	"An orphaned mammalian beta-globin gene of ancient evolutionary origin."
PROC.	Natl. Acad. Sci. U.S.A. 98:1101-1106 (2001).	DT	01-JUN-2001 (TREMBLel. 17, last sequence update)
CC	-!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.	DT	01-DEC-2001 (TREMBLel. 19, last annotation update)
EMBL	AV014769; AAK11484.1; -.	DE	HEMOGLOBIN, BETA ADULT MAJOR CHAIN.
DR	HSSP; P02112; 1HBR	GN	HBB-B1.
DR	InterPro; IPR002337; Beta_haem.	OS	Mus musculus (Mouse).
DR	InterPro; IPR000971; Globin.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR	InterPro; IPR02335; Myoglobin.	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DR	Pfam; PF00042; globin_1.	OX	NCBI_TAXID=10090;
DR	PRINTS; PR00014; BETAHAEM.	RN	[1]
DR	PRINTS; PR0013; MYOGLOBIN.	RP	SEQUENCE FROM N.A.
DR	PROSITE; PS01033; GLOBIN; 1.	RC	STRAIN=C57BL/6J; TISSUE=EMBRYONIC LIVER;
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	RX	MEDLINE=21085660; PubMed=11217851;
DR	SEQUENCE 147 AA; 16108 MW; 544D783F0B5BF488 CRC64;	RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RA	Akizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Kadoya K., Matsuda H.A., Ashburner M., Batyalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Q9BELL; PRELIMINARY; PRT; 147 AA.
DR	01-JUN-2001 (TREMBLel. 17, Created)	RA	Schrinri L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carnici P., de Roblo M.F., Brownstein M.J., Bult C., Fleicher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kanaiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibusawa Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming M., Wynshaw-Boris A., Yoshida K., Hasagawa Y., Kawaji H., Kohlbuski S., Hayashizaki Y.;
DR	01-JUN-2001 (TREMBLel. 17, Last sequence update)	RT	"Functional annotation of a full-length mouse cDNA collection.";
DT	01-DEC-2001 (TREMBLel. 19, Last annotation update)	RL	Nature 405:685-690 (2001).
DE	OMGC_GLOBIN.	CC	-!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
OS	Sminthopsis crassicaudata (Fat-tailed Dunnart).	DR	EMBL; AK010873; BA27237.1; -.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Sminthopsis.	DR	HSSP; P02423; IDXT.
OC	NCBI_TAXID=9301;	DR	MGD; MGII:96021; HBB-B1.
RN	[1]	DR	InterPro; IPR002337; Beta_haem.
RP	SEQUENCE FROM N.A.	DR	InterPro; IPR000971; Globin.
RX	MEDLINE=21107677; PubMed=11158601;	DR	InterPro; IPR002335; Myoglobin.
RA	Wheeler D., Hope R., Cooper S.J., Dolman G., Webb G.C., Bottema C.D., Gooley A.A., Goodman M., Holland R.A.;	DR	Pfam; PF00042; globin_1.
RA	"An orphaned mammalian beta-globin gene of ancient evolutionary origin.";	DR	PRINTS; PR00014; BETAHAEM.
RA	Proc. Natl. Acad. Sci. U.S.A. 98:1101-1106 (2001).	DR	PROSITE; PS01033; GLOBIN; 1.
CC	-!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.	DR	SEQUENCE 147 AA; 15778 MW; 79E4AFEBBAE95972 CRC64;
DR	EMBL; AK014770; AAK11485.1; -.	DR	HSSP; P02112; 1HBR.
DR	InterPro; IPR002337; Beta_haem.	DR	InterPro; IPR002337; Beta_haem.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; MYOGLOBIN.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; GLOBIN; 1.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; MYOGLOBIN.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; GLOBIN; 1.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; MYOGLOBIN.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; GLOBIN; 1.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; MYOGLOBIN.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; GLOBIN; 1.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; MYOGLOBIN.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; GLOBIN; 1.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; MYOGLOBIN.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; GLOBIN; 1.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; MYOGLOBIN.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; GLOBIN; 1.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; MYOGLOBIN.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; GLOBIN; 1.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; MYOGLOBIN.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; GLOBIN; 1.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR	PROSITE; PS01033; MYOGLOBIN.	DR	InterPro; IPR002335; Myoglobin.
DR	ERYTHROCYTE; Heme; oxygen transport; Respiratory protein.	DR	InterPro; IPR002335; Myoglobin.
DR	SEQUENCE 147 AA; 163550 MW; 47510F7C2D569B74 CRC64;	DR	InterPro; IPR002335; Myoglobin.
DR	Best Local Similarity 100.0%; Score 9; DB 6; Length 147; Pred. No. 0.0011; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InterPro; IPR002335; Myoglobin.
DR	InterPro; IPR000971; Globin.	DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.	DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.	DR	InterPro; IPR002335; Myoglobin.
DR	PRINTS; PR00014; BETAHAEM.	DR	InterPro; IPR002335; Myoglobin.
DR			

RP SEQUENCE FROM N A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC LIVER;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawaji J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Alzava K., Izawa M., Nishi K., Kiyocawa T., Saito R.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Rishburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzairelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1 SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AK011053; BAB27362.1; ..
 DR HSSP; P0203; IDXT.
 DR MGII; MGI:96021; Hbb; bl.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR002335; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PRO0814; BETAHAM.
 DR PRINTS; PRO0613; MYOGLOBIN.
 DR PROSTB; PS01033; GLOBIN; 1.
 DR Erythrocyte; Heme; oxygen transport; Respiratory protein.
 SQ SEQUENCE (13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY) (13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2510039D08, FULL INSERT SEQUENCE) (13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2510039M06, FULL INSERT SEQUENCE) (13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2510040107, FULL INSERT SEQUENCE) (13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2510039C09, FULL INSERT SEQUENCE) (13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2510040116, FULL INSERT SEQUENCE) (13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2510044F14, FULL INSERT SEQUENCE).
 OS MUS musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N A.
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY, SPLEEN, PLACENTA, AND LIVER;
 RA Adachi J., Alzava K., Akabira S., Akimura T., Aono H., Arai A.,
 RA Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoaka T., Hori F.,
 RA Imotani K., Ishii Y., Ichijo M., Izawa M., Kato H., Kawai J., Kojima Y.,
 RA Kono H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
 RA Nishi K., Nomura K., Numasaki R., Ohno M., Ozaki Y., Okido T.,
 RA Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
 RA Shibata K., Shiba Y., Shinagawa A., Shiraki T., Sobage Y.,
 RA Suzuki H., Tagami M., Takeawa A., Takahashi F., Tanaka T., Teijima Y.,
 RA Toyota T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N A.
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY, SPLEEN, PLACENTA, AND LIVER;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N A.
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY, SPLEEN, PLACENTA, AND LIVER;
 RX MEDLINE=927953; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [4]
 RP SEQUENCE FROM N A.
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY, SPLEEN, PLACENTA, AND LIVER;
 RX MEDLINE=2049374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itch M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RA Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N A.
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY, SPLEEN, PLACENTA, AND LIVER;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Alzava K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akimura J., Nishi K., Kitsumi T., Tasiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

	SQ	SEQUENCE	147 AA:	16396 MW;	79E874B4EFA13EA CRC64;
RA	Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,				
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,				
RA	Ozaki Y., Muromatsu M., Inoue Y., Kit A., Hayashizaki Y.;				
RT	*RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.;				
RL	Genome Res. 10:1757-1771(2000).				
DR	EMBL; AK012551; BAB2811.1; -				
DR	EMBL; AK002258; BAB21971.1; -				
DR	EMBL; AK002394; BAB22067.1; -				
DR	EMBL; AK003096; BAB22562.1; -				
DR	EMBL; AK003472; BAB22806.1; -				
DR	EMBL; AK005442; BAB24036.1; -				
DR	EMBL; AK005490; BAB24075.1; -				
DR	EMBL; AK005496; BAB24080.1; -				
DR	EMBL; AK010902; BAB27255.1; -				
DR	EMBL; AK010980; BAB27302.1; -				
DR	EMBL; AK010981; BAB27303.1; -				
DR	EMBL; AK010991; BAB27310.1; -				
DR	EMBL; AK010993; BAB27312.1; -				
DR	EMBL; AK011006; BAB27325.1; -				
DR	EMBL; AK011013; BAB27331.1; -				
DR	EMBL; AK011016; BAB27334.1; -				
DR	EMBL; AK011027; BAB27343.1; -				
DR	EMBL; AK011033; BAB27347.1; -				
DR	EMBL; AK011050; BAB27360.1; -				
DR	EMBL; AK011052; BAB27361.1; -				
DR	EMBL; AK011057; BAB27365.1; -				
DR	EMBL; AK011067; BAB27374.1; -				
DR	EMBL; AK011069; BAB27376.1; -				
DR	EMBL; AK011077; BAB27382.1; -				
DR	EMBL; AK011083; BAB27387.1; -				
DR	SEQUENCE 147 AA; 15748 MW; 6CF0EAEBF1F3E8D9 CRC64;				
Query Match	90.0%; Score 9; DB 11; Length 147;				
Best Local Similarity	100.0%; Pred. No. 0.0011; Mismatches 0; Indels 0; Gaps 0;				
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 LVVYPWTQR 9				
Db	33 LVVYPWTQR 41				
RESULT	55				
Q9IGF5	PRELIMINARY; PRT; 147 AA.				
ID	Q9YGF5				
AC	00YGF5; PRELIMINARY; PRT; 147 AA.				
DT	01-MAY-1999 (TREMBREL. 10, Created)				
DT	01-MAY-1999 (TREMBREL. 10, Last sequence update)				
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)				
DE	EMBRYONIC BETA-TYPE GLOBIN.				
OS	Oncorhynchus mykiss (Rainbow trout) (<i>Salmo gairdneri</i>)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Osteichthyes; Actinopterygii; Neopterygii; Teleostei; Enteleteostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.				
OC	Actinopterygii; Neopterygii; Teleostei; Enteleteostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.				
OX	NCBI_TaxID=8022;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Maruyama K., RT				
RA	"Rainbow Trout Embryonic beta-Type Globin.";				
RL	Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.				
CC	-1 SIMILARITY: BELONGS TO THE GLOBIN FAMILY.				
DR	EMBL; AB015450; BA34950.1; -				
DR	HSSP; P80044; IPXX.				
DR	InterPro; IPR002337; Beta-haem.				
DR	InterPro; IPR00071; Globin.				
DR	InterPro; IPR002335; Myoglobin.				
DR	Prints; PR00042; globin_1.				
DR	Prints; PR00013; BETAHEM.				
DR	Prints; PR00613; MYOGLOBIN.				
DR	Prints; PS00133; GLOBIN_1.				
KW	Erythrocyte; Heme; Oxygen transport; Respiratory protein.				
SEQUENCE	147 AA; 16556 MW; 6CEC71C7B88CD94 CRC64;				
RESULT	57				
Q9RUB8	PRELIMINARY; PRT; 147 AA.				
ID	Q9RUB8				
AC	Q9RUB8; PRELIMINARY; PRT; 147 AA.				
DT	01-JUN-2001 (TREMBREL. 17, Created)				
DT	01-JUN-2001 (TREMBREL. 17, Last sequence update)				
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)				
DE	BETANCP2.				
GN	BETANCP2II.				
GN	Notochetaria coriiceps (black rockcod).				
OC	Eularyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Enteleteostei; Neoteleostei.				
OC	Actinopterygii; Acanthopterygii; Percomorpha; Perciformes; Notothenioidei; Nototheniidae; Notothenia.				
OC	Notothenioidei; Nototheniidae; Notothenia.				
OX	NCBI_TaxID=8208;				
RN	[1]				
RP	SEQUENCE FROM N.A.				

SQ	SEQUENCE	163 AA;	17403 MW;	D024994DF19CD71E CRC64;
RA	Cocca E., Detrich H.W. III, Parker S.K., di Prisco G.;			"A cluster of four globin genes from the Antarctic fish Notothenia coriiceps.";
RT				
RL	J. Fish Biol. 57:33-50(2000);			
CC	-!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.			
DR	EMBL; AF230741; AAK12630_1.; -.			
DR	HSSP; P80044; 1PBX;			InterPro; IPR002337; Beta_haem.
DR	InterPro; IPR000971; Globin.			
DR	Pfam; PF00042; globin_1.			
DR	PRINTS; PRO0814; BETAHEM.			
DR	PROSITE; PS01033; GLOBIN; 1.			
KW	Erythrocyte; Heme; Oxygen transport; Respiratory protein.			
SQ	SEQUENCE	147 AA;	16481 MW;	4AA39E1ECIBC89DE CRC64;
Query Match	90.0%; Score 9;	DB 13;	Length 147;	
Best Local Similarity	100.0%; Pred. No. 0.0011;			Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
OY	1 LVVYPWTQR 9			
Db	33 LVVYPWTQR 41			
RESULT	58			
09CXZ2	PRELIMINARY;	PRT;	163 AA.	
ID	09CXZ2			
AC	09CXZ2_01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	13 DANS EMBRYO CDNA; RIKEN FULL-LENGTH ENRICHED LIBRARY,			
DE	CLONE: 2510049H02, FULL INSERT SEQUENCE.			
GN	HBB-B1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID:10090;			
RN	[1]			
RP	SEQUENCE FROM N A.			
RX	STRAIN=C57BL/6J; TISSUE=EMBRYONIC LIVER;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanska I., Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Blakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blakai J., Boffelli D., Burjano G., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mazzarelli J., Montaigu P., Nordone P., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Storch K.-F., Suzuki H., Toyo-oka K., Wang H.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S., Hayashizaki Y.,			
RA	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:65-69(2001).			
CC	-!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.			
DR	EMBL; AK011119; BAB27413_1.; -.			
DR	HSSP; P02023; 1DXT; MG1; M61021; Hb; b1.			
DR	InterPro; IPR002337; Beta_haem.			
DR	InterPro; IPR000971; Globin.			
DR	Pfam; PF00042; globin_1.			
DR	PRINTS; PRO0814; BETAHEM.			
DR	PROSITE; PS01033; GLOBIN; 1.			
KW	Erythrocyte; Heme; Oxygen transport; Respiratory protein.			
RESULT	59			
090594	PRELIMINARY;	PRT;	15 AA.	
ID	090594			
AC	090594_01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-JAN-1999 (TREMBLrel. 09, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	GLOBIN (FRAGMENT).			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
OC	NCBI_TaxID:9031;			
RN	[1]			
RP	SEQUENCE FROM N A.			
RX	MEDLINE=81261952; PubMed=6266925;			
RA	Padayatty J., Cummings T., Manske C.L., Higuchi R., Woo S., Salser W., "Cloning of chicken globin cDNA in bacterial plasmids.";			
RT	Gene 13:417-422(1981).			
RL	-!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.			
CC	Gene 13:417-422(1981).			
DR	EMBL; M10380; AA048803_1.; -.			
DR	InterPro; IPR000971; Globin.			
DR	PROSITE; PS01033; GLOBIN; 1.			
KW	Heme; Oxygen transport; Respiratory protein.			
FT	NON_TER 1 1 1			
FT	NON_TER 15 15 15			
FT	NON_TER 15 15 15			
SQ	SEQUENCE	15 AA;	1881 MW;	23E61DA734FA7962 CRC64;
Query Match	80.0%; Score 8;	DB 13;	Length 15;	
Best Local Similarity	100.0%; Pred. No. 0.0027;			Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
OY	3 VYPWTQR 10			
Db	6 VYPWTQR 13			
RESULT	60			
09BE00	PRELIMINARY;	PRT;	31 AA.	
ID	09BE00			
AC	09BE00_01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	OMEGA GLOBIN (FRAGMENT).			
OS	Monodelphis domestica (Short-tailed grey opossum);			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Monodelphis.			
OC	NCBI_TaxID:13616;			
RN	[1]			
RP	SEQUENCE FROM N A.			
RX	MEDLINE=21107677; PubMed=11158601;			
RA	Wheeler D., Hope R., Cooper S.J., Dolman G., Webb G.C., Bottema C.D., Gooley A.A., Goodman M., Holland R.A.;"An orphaned mammalian beta-globin gene of ancient evolutionary origin.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 98:1101-1106(2001).			
RL	-!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.			
CC	Proc. Natl. Acad. Sci. U.S.A. 98:1101-1106(2001).			
DR	EMBL; AY014771; AAK11486_1.; -.			
DR	HSSP; P02096; 1FDH.			

DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PROSITE; PS0103; GLOBIN; 1.
 KW Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 1 1
 SQ SEQUENCE 31 AA; 3547 MW; 0353D72F3681617D CRC64;
 Query Match 80.0%; Score 8; DB 6; Length 31;
 Best Local Similarity 100.0%; Pred. No. 0.005; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTQ 8
 Db 24 LVVYPWTQ 31

RESULT 61
 PRELIMINARY; PRT; 61 AA.
 ID 099M06
 AC 099M06
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ADULT BETA MAJOR GLOBIN (FRAGMENT).
 OS Cricetulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetidae.
 OX NCBI_TAXID=10029;
 RN [1]
 RP SEQUENCE FROM N_A.
 RX MEDLINE=21363566; PubMed=11470918;
 RA Li F., Chen J., Izumi M., Butler M.C., Keezer S.M., Gilbert D.M.;
 RT "The replication timing program of the Chinese hamster beta-globin locus is established coincident with its repositioning near peripheral heterochromatin in early G1 phase.";
 RL J Cell Biol. 154:283-292(2001).
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; AF314661; AAC19259; 1; -.
 DR HSSP; P0203; TABW
 DR InterPro; IPR003337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PRO0814; BETAHAEV.
 DR PROSITE; PS01033; GLOBIN; 1.
 DR ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
 KW Peromyscus maniculatus (Deer mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Peromyscus.
 OX NCBI_TAXID=10042;
 RN [1]
 RP SEQUENCE FROM N_A.
 RX MEDLINE=88188975; PubMed=3447002;
 RA Padgett R.W., Loeb D.D., Snyder L.R.G., Edgell M.H., Hutchison C.A. III;
 RT "The molecular organization of the beta-globin complex of the deer mouse, Peromyscus maniculatus.";
 RL Mol. Biol. Evol. 4:30-45(1987).
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; M15296; AAC40595; 1; -.
 DR InterPro; IPR02337; Beta_haem.
 DR InterPro; IPR003337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PRO0814; BETAHAEV.
 DR PROSITE; PS01033; GLOBIN; 1.
 DR ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
 KW Peromyscus maniculatus (Deer mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Query Match 80.0%; Score 8; DB 11; Length 61;
 Best Local Similarity 100.0%; Pred. No. 0.0087; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 VPPWTQRF 10
 Db 4 VPPWTQRF 11

RESULT 63
 PRELIMINARY; PRT; 73 AA.
 ID 062586
 AC 062586
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE (DEER MOUSE) BETA-3-GLOBIN (HBB-B3) DNA, SECOND CODING-BLOCK REGION (FRAGMENT).
 OS Peromyscus maniculatus (Deer mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Peromyscus.
 OX NCBI_TAXID=10042;
 RN [1]
 RP SEQUENCE FROM N_A.
 RX MEDLINE=88188975; PubMed=3447002;
 RA Padgett R.W., Loeb D.D., Snyder L.R.G., Edgell M.H., Hutchison C.A. III;
 RT "The molecular organization of the beta-globin complex of the deer mouse, Peromyscus maniculatus.";
 RL Mol. Biol. Evol. 4:30-45(1987).
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; M15296; AAC40595; 1; -.
 DR HSSP; P02070; 1HDA.
 DR InterPro; IPR02337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PRO0814; BETAHAEV.
 DR PROSITE; PS01033; GLOBIN; 1.
 DR ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
 KW Peromyscus maniculatus (Deer mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Query Match 80.0%; Score 8; DB 11; Length 73;
 Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 VPPWTQRF 10
 Db 4 VPPWTQRF 11

RESULT 62
 PRELIMINARY; PRT; 73 AA.
 ID 064372
 AC 064372
 DT 01-NOV-1995 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE (DEER MOUSE) BETA-2-GLOBIN (HBB-B2) DNA, SECOND CODING-BLOCK REGION (FRAGMENT).
 DE PARTIAL CDS (FRAGMENT).
 OS Peromyscus maniculatus (Deer mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TAXID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHEJU NATIVE HORSE;
 RA Kim G.O.; Kim S.J.; Kim K.I.; Oh M.Y.;
 RT "Isolation and characterization of epsilon-1 gene in Cheju native
 horse.";
 RL Submitted (SRP-1996) to the EMBL/Genbank/DDBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; U0986; AAB16849.1; -.
 DR HSSP; P02100; 1A9W.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR InterPro; IPR002335; Myoglobin.
 DR Pfam; PF0042; globin_1.
 DR Pfam; PF0042; globin_1.
 DR PRINTS; PR00814; BETAHEM.
 DR PRINTS; PR00813; MYOGLOBIN.
 DR PROSITE; PS0103; GLOBIN.
 DR ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 106 AA; 11663 MW; B7EED1OB53448B1F CRC64;
 SEQUENCE 106 AA; 11663 MW; B7EED1OB53448B1F CRC64;

Query Match 80.0%; Score 8; DB 6; Length 106;
 Best Local Similarity 100.0%; Pred. No. 0.014; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQ 8
 |||||
 Db 33 LVVYPWTQ 40

RESULT 68
 ID 09c2g2 PRELIMINARY; PRT; 125 AA.

AC 09c2g2; PRELIMINARY;
 DT 01-JUN-2001 (TREMBrel. 17, Created)
 DT .01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE 10..11 DAYS EMBRYO cDNA, RIKEN FULL LENGTH ENRICHED LIBRARY,
 DE CLONE:231003C03 FULL INSERT SEQUENCE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR;
 RA Stevanovic M.J.; Crkvenjakov R.;
 RL Submitted (JUN-1991) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; X60730; CAA45138.1; -.
 DR HSSP; P02100; 1A9W.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR002335; Myoglobin.
 DR Pfam; PF0042; globin_1.
 DR PRINTS; PR00814; BETAHEM.
 DR PRINTS; PR00813; MYOGLOBIN.
 DR PROSITE; PS0103; GLOBIN.
 DR ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 135 AA; 15257 MW; 2C776CF27A9FDE27 CRC64;
 SEQUENCE 135 AA; 15257 MW; 2C776CF27A9FDE27 CRC64;

Query Match 80.0%; Score 8; DB 11; Length 135;
 Best Local Similarity 100.0%; Pred. No. 0.017; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VWPWTQRF 10
 |||||
 Db 35 VWPWTQRF 42

RESULT 70
 ID 061600 PRELIMINARY; PRT; 140 AA.

AC 061600; PRELIMINARY;
 DT 01-Nov-1996 (TREMBrel. 01, Created)
 DT 01-Nov-1996 (TREMBrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE BETA-H1-GLOBIN (FRAGMENT).
 DR HBB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=8829090; PubMed=2444404;
RA	Wilkinson D.G., Bailes J.A., Champion J.E., McMahon A.P.;
RT	"A molecular analysis of mouse development from 8 to 10 days post coitus detects changes only in embryonic globin expression.",
RL	Development 99:493-500 (1987).
CC	-1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
EMBL	M25894; AAA37695.1; -
DR	HSSP; P02056; 1FDH.
DR	MGD; MGI:98020; Hbb.
DR	InterPro; IPR002337; Beta_haem.
DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.
DR	PRINTS; PRO0814; BETAHAEM.
DR	PROSITE; PS0103; GLOBIN_1.
KW	Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT	NON_TER 1
FIT	SEQUENCE 140 AA; 15644 MW; 304B3F8522C666F5 CRC64;
RN	[1]
Query Match	80.0%; Score 8; DB 11; Length 140;
Best Local Similarity	100.0%; Pred. No. 0.017; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches	0;
QY	3 VYPWTORF 10
Db	34 VYPWTORF 41
RESULT	72
PRELIMINARY:	PRT; 147 AA.
RC	STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX	Medline=21085660; Pubmed=11218851;
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cassavant T., Fleischmann R., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido T., Pesole G., Quackenbush J., Schirmer L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Rinewald M., Rodriguez J., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seye T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.,
RA	"Functional annotation of a full-length mouse cDNA collection.",
RT	Nature 409:685-690(2001).
RL	-1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC	EMBL; AK012495; BAB28280.1; -
DR	HSSP; P02100; 1A9W.
DR	MGD; MGI:96024; Hbb_bh1.
DR	InterPro; IPR002337; Beta_haem.
DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.
DR	PRINTS; PRO0814; BETAHAEM.
DR	PROSITE; PS0103; GLOBIN_1.
KW	Heme; Oxygen transport; Erythrocyte; Metal-binding; Transport.
FT	METAL 63 63 (BY SIMILARITY).
FT	IRON (HEME PROXIMAL LIGAND)
METAL	92 92 (BY SIMILARITY).
FT	IRON (HEME DISTAL LIGAND)
SEQUENCE	146 AA; 16174 MW; A66CB0866946902F CRC64;
RN	[1]
Query Match	80.0%; Score 8; DB 11; Length 147;
Best Local Similarity	100.0%; Pred. No. 0.018; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches	0;
QY	3 VYPWTORF 10
Db	35 VYPWTORF 42
RESULT	73
PRELIMINARY:	PRT; 147 AA.
RC	STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX	Medline=21085660; Pubmed=11218851;
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cassavant T., Fleischmann R., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido T., Pesole G., Quackenbush J., Schirmer L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Rinewald M., Rodriguez J., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seye T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.,
RA	"Functional annotation of a full-length mouse cDNA collection.",
RT	Nature 409:685-690(2001).
RL	-1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC	EMBL; AK012495; BAB28280.1; -
DR	HSSP; P02100; 1A9W.
DR	MGD; MGI:96024; Hbb_bh1.
DR	InterPro; IPR002337; Beta_haem.
DR	InterPro; IPR000971; Globin.
DR	InterPro; IPR002335; Myoglobin.
DR	Pfam; PF00042; globin_1.
DR	PRINTS; PRO0814; BETAHAEM.
DR	PROSITE; PS0103; GLOBIN_1.
KW	Heme; Oxygen transport; Erythrocyte; Metal-binding; Transport.
FT	METAL 63 63 (BY SIMILARITY).
FT	IRON (HEME PROXIMAL LIGAND)
METAL	92 92 (BY SIMILARITY).
FT	IRON (HEME DISTAL LIGAND)
SEQUENCE	146 AA; 16174 MW; A66CB0866946902F CRC64;
RN	[1]
Query Match	80.0%; Score 8; DB 11; Length 147;
Best Local Similarity	100.0%; Pred. No. 0.018; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches	0;
QY	3 VYPWTORF 10
Db	35 VYPWTORF 42

RX MEDLINE=91140361; PubMed=8307571;
 RA Reitman M., Grasso J.A., Blumenthal R., Lewit P.;
 RT "Primary sequence, evolution and repetitive elements of the Gallus
 RT gallus (chicken) beta-globin cluster.";
 RL Genomics 18:616-626(1993).
 -I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: L17432; RADD3346.1; -.
 DR HSSP: P02112; IHBH.
 DR InterPro: IPR002337; Beta-haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINS: PR00814; BEPAHAEM.
 DR PROSITE: PS0103; GLOBIN; 1.
 KW ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE: 147 AA; 16365 MW; C933A2810304AD9C CRC64;

Query Match 80.0%; Score 8; DB 13; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.018; 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VWPWTQRF 10
 Db 35 VWPWTQRF 42

RESULT 77
 Q90938 PRELIMINARY; PRT; 147 AA.
 AC 090938;
 DT 01-NOV-1996 (TREMBREL_01, created)
 DT 01-NOV-1996 (TREMBREL_01, last sequence update)
 DE 01-DEC-2001 (TREMBREL_19, last annotation update)
 CC MRNA, COMPLETE ORF
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Larrick J.W., Espinoza D.O.;
 RT "Mutant hemoglobin (Beta chain thr 69->ser) with high oxygen affinity
 from Gallus gallus native to the altiplano of Peru.";
 RT Submitted (JAN-1992) to the EMBL/GenBank/DDBJ databases.
 -I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: M73955; AAA4896.1; -.
 DR HSSP: P02112; IHBH.
 DR InterPro: IPR002337; Beta-haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINS: PR00814; BEPAHAEM.
 DR PROSITE: PS0103; GLOBIN; 1.
 DR ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
 KW SEQUENCE: 147 AA; 16452 MW; F0E3972C6DE73428 CRC64;

Query Match 70.0%; Score 7; DB 4; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.13; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VWPWTQRF 10
 Db 36 VWPWTQRF 42

RESULT ?9
 Q9PWHT PRELIMINARY; PRT; 69 AA.
 AC 09PWHT;
 DT 01-MAY-2000 (TREMBREL_13, created)
 DT 01-MAY-2000 (TREMBREL_13, last sequence update)
 DE BETA_GLOBIN (FRAGMENT).
 GN SB-B2
 OS Morone saxatilis (Striped bass).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
 OC Moronidae; Morone.
 OC NCBI_TaxID=34816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hiroko I., Aoki T., Powers D.A.;
 RT "Characterization of the alpha and beta globin genes of striped bass,
 RT Morone saxatilis.";
 RT Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 CC -I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AB023443; BAAB2806.1; -.
 DR HSSP: P80044; IHBH.
 DR InterPro: IPR002337; Beta-haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINS: PR00814; BEPAHAEM.
 DR PROSITE: PS0103; GLOBIN; 1.
 KW ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 1 1
 FT SEQUENCE 69 AA; 7715 MW; AA489BABAEB55E0E CRC64;

Query Match 70.0%; Score 7; DB 13; Length 69;

Qy 3 VWPWTQRF 10
 ID 095408 PRELIMINARY; PRT; 57 AA.
 AC 095408; |||||||
 Db 35 VWPWTQRF 42

RESULT 78
 Q95408 VWPWTQRF 10
 ID 095408 PRELIMINARY; PRT; 57 AA.
 AC 095408; |||||||
 DT 01-MAY-1999 (TREMBREL_10, created)
 DT 01-MAY-1999 (TREMBREL_10, last sequence update)
 DT 01-DEC-2001 (TREMBREL_19, last annotation update)

DE BETA_GLOBIN (FRAGMENT).
 GN HBB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_TaxID=9605;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RA Kutlar F., Wilson J., Wenk R.E., Luddy R., Holley L., Markowitz R.,
 RA Kutlar A.;
 RT "Hemoglobin Sinal-Greenspring, a new silent GTC 34 ATC mutation of
 RT human beta globin gene.", Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
 CC -I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AF104901; AAC97372.1; -.
 DR HSSP; P02023; IDXT.
 DR InterPro: IPR002337; Beta-haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINS: PR00814; BEPAHAEM.
 DR PROSITE: PS0103; GLOBIN; 1.
 KW ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
 FT VARIANT: 35 35
 FT NON_TER 57 57
 FT SEQUENCE 57 AA; 6266 MW; FDC12A13A9D35934 CRC64;

QY	3	VWPWTQR 9	Best Local Similarity 100.0%; Pred. No. 0.16; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	2	VWPWTQR 8	
RESULT	80		
09FWH5		PRELIMINARY;	PRT; 69 AA.
ID	09FWH5		
AC	09FWH5:		01-MAY-2000 (TREMBrel. 13, Created)
DT	01-MAY-2000 (TREMBrel. 13, Last sequence update)		
DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)		
DE	BETA GLOBIN (FRAGMENT).		
GN	SB-B4.		
OS	Morone saxatilis (Striped bass).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoides;		
OX	Moronidae; Morone.		
RN	[1]		SEQUENCE FROM N.A.
RP	Hirono T., Aoki T., Powers D.A.;		
RA	Hirono T., Aoki T., Powers D.A.;		
RT	"Characterization of the alpha and beta globin genes of striped bass,"		
RT	Morone saxatilis,"; to the EMBL/GenBank/DBJ databases.		
RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.		
-!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.			
DR	EMBL; AB023445; BAA82808.1; .		
DR	HSPP; P80044; 1BHB.		
DR	InterPro; IPR002337; Beta_haem.		
DR	InterPro; IPR000971; Globin.		
PRNT	PF00042; globin_1.		
DR	PRINTS; PR00814; BETAHAE.		
DR	PROSITE; PS01033; GLOBIN; 1.		
KW	Erythrocyte; Heme; Oxygen transport; Respiratory protein.		
FT	NON_TER 1 69		
FT	NON_TER 69 69		
SQ	SEQUENCE 69 AA; 7767 MW; 0B6B5E632991CICA CRC64;		
Query Match 70.0%; Score 7; DB 13; Length 69; Best Local Similarity 100.0%; Pred. No. 0.16; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OS PROSITE; PS01033; GLOBIN; 1.			
QY	3	VWPWTQR 9	
Db	2	VWPWTQR 8	
RESULT	81		
09O488		PRELIMINARY;	PRT; 105 AA.
ID	09O488:		
AC	09O488:		01-NOV-1996 (TREMBrel. 01, Created)
DT	01-NOV-1996 (TREMBrel. 01, Last sequence update)		
DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)		
DE	BETA GLOBIN (FRAGMENT).		
OS	Brachydanio rerio (zebrafish) (Zebra danio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi;		
OC	Cypriniformes; Cyprinidae; Danio.		
OX	NCBI_TaxID=7955;		
RN	[1]		SEQUENCE FROM N.A.
RP	ZON L.;		
RL	Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.		
CC	-!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.		
DR	EMBL; 050382; AAC05405.1; -.		
DR	PRINTS; PR00814; BETAHAE.		
DR	InterPro; IPR002337; Beta_haem.		
RESULT	83		
09DOB2		PRELIMINARY;	PRT; 147 AA.
ID	09DOB2:		
AC	09DOB2:		01-JUN-2001 (TREMBrel. 17, Created)
DT	01-JUN-2001 (TREMBrel. 17, Last sequence update)		
DT	01-JUN-2001 (TREMBrel. 19, Last annotation update)		
DE	HEMOGLOBIN Y, BETA-LIKE EMBRYONIC CHAIN.		
GN	HBB-Y.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		

Qy 3 VYPWTQR 9
 |||||
 ID 062670 PRELIMINARY; PRT; 147 AA.
 AC 062670;
 DT 01-NOV-1996 (TREMBrel. 01, Created)
 DR 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE 0 BETA-2 GLOBIN.
 GN 0 BETA-2 GLOBIN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR; TISSUE=LIVER;
 RA Inokuchi N.; Iwahara S.I.; Satoh H.; Nagoe Y.; Okazaki T.;
 RT "Organization structure and expression of rat beta-globin genes.";
 RL Submitted (JUL-1992) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: X67617; CAA47877.1; -.
 DR HSSP: P02023; IDXT.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin_1.
 DR PRINTS: PRO0814; BETAHEM.
 DR PROSITE: PS01033; GLOBIN_1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 147 AA; 15979 MW; 93BB045CC26D57BA CRC64;

Qy 3 VYPWTQR 9
 |||||
 ID 09YGF4 PRELIMINARY; PRT; 147 AA.
 AC 09YGF4;
 DT 01-MAY-1999 (TREMBrel. 10, Created)
 DR 01-MAY-1999 (TREMBrel. 10, Last sequence update)
 DE EMBRYONIC BETA-TYPE GLOBIN2.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopercy91; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maruyama K.;
 RT Rainbow trout Embryonic beta-type Globin2."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AB015451; BAA34951.1; -.
 DR HSSP: P80044; IPKX.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin_1.
 DR PRINTS: PRO0814; BETAHEM.
 DR PROSITE: PS01033; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN_1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 147 AA; 16655 MW; D7CBC5F971762E8 CRC64;

RESULT 87
 Q91470 PRELIMINARY; PRT; 147 AA.
 ID 091470
 AC 091470; 013233; 013185;
 DT 01-NOV-1996 (TREMBrel. 01, Created)
 DR 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-OCT-2001 (TREMBrel. 18, Last annotation update)
 DE BETA-GLOBIN.
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopercy91; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A.; PubMed=8924215;
 RX MEDLINE=96211166; PubMed=8924215;
 RA McMorrow T.; Wagner A.; Deycckere F.; Gannon F.;
 RT "Structural organization and sequence analysis of the globin locus in
 Atlantic salmon.";
 RL DNA Cell Biol. 15:407-414(1996).
 RN [2]
 RP SEQUENCE FROM N.A.;
 RX MEDLINE=97311408; PubMed=9168125;
 RA McMorrow T.; Wagner A.; Harte T.; Gannon F.;
 RT "Sequence analysis and tissue expression of a non-Bohr beta-globin
 cDNA from Atlantic salmon.";
 RL Gene 189:183-188(1997).

Qy 3 VYPWTQR 9
 |||||
 ID 09YGF8 PRELIMINARY; PRT; 147 AA.
 AC 09YGF8;
 DT 01-MAY-2000 (TREMBrel. 13, Created)
 DR 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE LARVAL BETA-GLOBIN.
 OS Hyphobius retardatus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Cryptobranchidae; Hyphobidae; Hyphobius.
 OX NCBI_TaxID=36312;

RN	[1]
RP	SEQUENCE FROM N.A.
RA	Yanaguchi M., Takahashi H., Wakahara M.;
RT	"Erythropoiesis and unexpected expression pattern of globin genes in the salamander <i>Hynobius retardatus</i> .";
RL	Dev. Genes Evol. 0-0-01999;
CC	-! SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR	EMBL; AR034757; JAF;
DR	HSSP; P02118; JAF;
DR	InterPro; IPR002337; Beta_haem.
DR	InterPro; IPR000971; Globin.
DR	Pfam; PF00042; globin; 1.
DR	PRINTS; PR00814; BETAHAE.
DR	PROSITE; PS01033; GLOBIN; 1.
KW	Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ	SEQUENCE 147 AA; 16006 MW; A96F1D05A4AD4727 CRC64;
Query Match	70.0%; Score 7; DB 13; Length 147;
Best Local Similarity	100.0%; Pred. No. 0.29;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	3 VYPWTQR 9
Db	35 VYPWTQR 41
RESULT	90
ID	093548
AC	093548;
DT	01-NOV-1998 (TREMBlrel. 08, Created)
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE	01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN	BETA-GLOBIN.
OS	Brachydanio rerio (Zebrafish) (zebra danio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Teleostei; Euteleostei; Ostariophysi; Osteichthyes; Cypriniformes; Cyprinidae; Danio.
OX	NCBI_TAXID=7955;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE:99147139; PubMed=10022956;
RA	Quinkertz A., Campos-Ortega J.A.;
RT	"A new beta-globin gene from the zebrafish, betaEl, and its pattern of transcription during embryogenesis.;"
RL	Dev. Genes Evol. 209:126-131 (1999).
CC	-! SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR	EMBL; AF084662; AAC62069.1; -.
DR	HSSP; P80044; 1PBX.
DR	InterPro; IPR002337; Beta_haem.
DR	InterPro; IPR000971; Globin.
DR	Pfam; PF00042; globin; 1.
DR	PRINTS; PR00814; BETAHAE.
DR	PROSITE; PS01033; GLOBIN; 1.
KW	Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ	SEQUENCE 147 AA; 16200 MW; 615CB02B8804009F4 CRC64;
Query Match	70.0%; Score 7; DB 13; Length 147;
Best Local Similarity	100.0%; Pred. No. 0.29;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	3 VYPWTQR 9
Db	35 VYPWTQR 41
RESULT	92
ID	091471
AC	091471;
DT	01-NOV-1996 (TREMBlrel. 01, Created)
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE	BETA-GLOBIN.
OS	Salmo salar (Atlantic salmon).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Salmonidae; Salmo.
OX	NCBI_TAXID=8030;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE:96211166; PubMed=8924215;
RA	"Structural organisation and sequence analysis of the globin locus from Atlantic salmon.;"
RL	Cell Biol. 15:407-414 (1996).
CC	-! SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR	EMBL; X97287; CA05590.1; -.
DR	HSSP; P02142; IOUT;
DR	InterPro; IPR000971; Globin.
DR	Pfam; PF00042; globin; 1.
KW	Heme; Oxygen transport; Respiratory protein.
SQ	SEQUENCE 147 AA; 15971 MW; CD5FBELF9060E19 CRC64;
Query Match	70.0%; Score 7; DB 13; Length 147;
Best Local Similarity	100.0%; Pred. No. 0.29;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	3 VYPWTQR 9
Db	35 VYPWTQR 41
Query Match	70.0%; Score 7; DB 13; Length 147;
Best Local Similarity	100.0%; Pred. No. 0.29;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	3 VYPWTQR 9

Db	55 VVPWTQQR 41	Matches	7;	conservative	0;	Mismatches	0;	indels	0;	gaps
RESULT	93									
091129		PRELIMINARY;	PRT;	147 AA.						
ID	091129									
AC	091129;									
DT	01-NOV-1996 (TREMBLrel. 01, Created)									
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)									
DE	BETA-GLOBIN.									
DE	Notothenia corriceps (black rockcod).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;									
OC	Actinopterygii; Acanthopterygii; Percormorpha; Perciformes; Notothenioidei; Nototheniidae; Notothenia.									
OX	NCBI_TaxID=8208;									
RN	[1] SEQUENCE FROM N.A.									
RX	MEDLINE=95119244; PubMed=7892183;									
RA	Coccia E.; Ratnayake-Lecanawasam M.; Parker S.K.; Camardella L.,									
RA	Clarmella M.; di Prisco G.; Detrich H.W. III;									
RT	"Genomic remnants of alpha-globin genes in the hemoglobinless antarctic icefishes;"									
RL	PROC. NATL ACAD SCI U S A. 92:1817-1821(1995).									
CC	-! SIMILARITY: BELONGS TO THE GLOBIN FAMILY.									
EMBL	U09187; AAC61202.1; -.									
DR	HSSP_P80044; 1P BX.									
DR	InterPro; IPR002337; Beta-haem.									
DR	InterPro; IPR000971; Globin.									
DR	Pfam; PF00042; globin; 1.									
DR	PRINTS; PR00814; BETAHEM.									
DR	PROSITE; PS01033; GLOBIN; 1.									
KW	Erythrocyte; Heme; Oxygen transport; Respiratory protein.									
SQ	SEQUENCE 147 AA; 16316 MW; 966A33B9878D5D22 CRC64;									
Query	Match	70.0%	Score	7;	DB	13;	Length	147;		
Best	Local Similarity	100.0%	Pred.	No.	0.29;					
Matches	7;	Conservative	0;	Mismatches	0;					
Indels	0;	Gaps	0;							
QY	3 VVPWTQQR 9									
Db	35 VVPWTQQR 41									
RESULT	94									
090ZM4	PRELIMINARY;	PRT;	147 AA.							
ID	090ZM4;									
AC	090ZM4;									
DT	01-DEC-2001 (TREMBLrel. 19, Created)									
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)									
DE	HEMOGLOBIN BETA CHAIN.									
OS	Epinephelus cooides (orange-spotted grouper).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Notoleosteii; Acanthomorphia; Acanthopterygii; Percomorpha; Perciformes; Pocoidei; Seritidae; Epinephelus.									
OX	NCBI_TaxID=94223;									
RN	[1] SEQUENCE FROM N.A.									
RP	Yin Z.X., He J.G., Ye Q.Z., Wang S.P., Zhai Y.L.;									
RT	"Cloning and sequencing of hemoglobin beta gene of orange-spotted grouper (Epinephelus cooides)."; Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.									
RL	Submitter (APR-2001) to the EMBL/GenBank/DBJ databases.									
DR	EMBL:AY029506; AAK38736.1; -.									
DR	SEQUENCE 147 AA; 16544 MW; EC389C1010ECDFFC CRC64;									
Query	Match	70.0%	Score	7;	DB	13;	Length	147;		
Best	Local Similarity	100.0%	Pred.	No.	0.29;					
Local	Similarity	100.0%	Pred.	No.	0.29;					

RT "Analysis of alpha-globin gene family of carp. I. alpha-globin gene
 RT structure of No.3, No.6, and No.7.";
 RL Nippon Suisan Gakkaishi 59:1077-1083(1993).
 CC -I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 EMBL: AB004740; BAA20516.1; -.
 DR HSSP: P56251; ISPG.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; Globin; 1.
 PRINTS: PRO00814; BETAHAEAM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 148 AA; 16343 MW; 42D2B816F9B6FEA3 CRC64;

Query Match 70.0%; Score 7; DB 13; Length 148;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 VYPWTQ9 9
 |||||
 Db 35 VYPWTQR 41

RESULT 97
 ID Q98851 PRELIMINARY; PRT; 148 AA.
 AC Q98851;
 DT 01-FEB-1997 (TREMBrel. 02, Created)
 DT 01-FEB-1997 (TREMBrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE BETA-GLOBIN
 OS Cyprinus carpio (common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprinus.
 OX NCBI_TaxID:7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yoshizaki G.;
 RT "Cloning and sequencing of adult carp beta-globin family cDNA.";
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: D88116; BRA13536.1; -.
 DR HSSP; P56251; ISPG.
 DR InterPro; IPR002337; Beta_haem.
 DR Pfam; PF00042; globin; 1.
 PRINTS: PRO00814; BETAHAEAM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW ERYTHROCYTE; Heme; Oxygen transport; Respiratory Protein.
 SQ SEQUENCE 148 AA; 16371 MW; 42CC68F85B6FEA3 CRC64;

Query Match 70.0%; Score 7; DB 13; Length 148;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 VYPWTQ9 9
 |||||
 Db 35 VYPWTQR 41

RESULT 98
 ID Q98852 PRELIMINARY; PRT; 148 AA.
 AC Q98852;
 DT 01-FEB-1997 (TREMBrel. 02, Created)
 DT 01-FEB-1997 (TREMBrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE BETA-GLOBIN
 OS Cyprinus carpio (Common carp).
 SQ SEQUENCE FROM N.A.

Query Match 70.0%; Score 7; DB 13; Length 148;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 VYPWTQ9 9
 |||||
 Db 35 VYPWTQR 41

RESULT 100
 ID Q90485 PRELIMINARY; PRT; 148 AA.
 AC Q90485;
 DT 01-Nov-1996 (TREMBrel. 01, Created)

OC Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprinus.
 NCBI_TaxID:7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yoshizaki G.;
 RT "Cloning and sequencing of adult carp beta-globin family cDNA.";
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: D88119; BRA13539.1; -.
 DR HSSP; P56251; ISPG.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 PRINTS: PRO00814; BETAHAEAM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW ERYTHROCYTE; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 148 AA; 16482 MW; 03C69F098BD3ETCF CRC64;

DT 01-NOV-1996 (TREMBrel. 01, last sequence update.)
DT 01-DEC-2001 (TREMBrel. 19, last annotation update.)
DE BA2 GLOBIN.
GN BA2 OR BA2.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID:7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Zou L.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
CC -1 SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; U50379; AAB05402.1; -.
DR HSSP; P56231; ISPAG.
DR ZFIN; ZDB-GENE:990415-19; ba2.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BEIAHAE.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; oxygen transport; Respiratory protein.
SQ SEQUENCE 148 AA; 16389 MW; BC35853B7EC14 CxG64;

Query Match 70.0%; Score 7; DB 13; Length 148;
Best Local Similarity 100.0%; Pred. No. 0.29; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VIFFWTQR 9
Db 35 VIFFWTQR 41

Search completed: July 1, 2002, 12:10:33
Job time: 221 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 12:06:27 ; Search time 30.01 Seconds
(without alignments)

37.012 Million cell updates/sec

Title: US-09-147-490-1
Perfect score: 10
Sequence: 1 LVVPPWTFQRF 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues
Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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20: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA2000.DAT: *
21: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA2001.DAT: *22: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA2001.DAT: *Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	#		
Result No.	Score	Query	Match Length	DB ID	Description
1	100.0	10 17 AAR97348	17	AAR97348	Peptide fragment o
2	100.0	10 18 AAW30318	18	AAW30318	Peptide haemorphin
3	100.0	10 19 AAW37247	19	AAW37247	Angiotensin IV act
4	100.0	6 AAP50291	74	AAP50291	Sequence encoded b
5	100.0	74 16 AAR69602	16	AAR69602	Human beta-globin
6	100.0	86 22 AAR07245	22	AAR07245	Human polyPeptide
7	100.0	104 22 AAU30074	22	AAU30074	Novel human secret
8	100.0	110 22 AAQ02538	22	AAQ02538	Human polypeptide
9	100.0	112 16 AAR89262	16	AAR89262	Human beta-globin
10	100.0	112 16 AAR89261	16	AAR89261	Human beta-globin
11	100.0	121 21 AAG01752	21	AAG01752	Human secreted pro

12 10 100.0 124 22 AAU29698 Novel human secret
13 10 100.0 127 22 AAO13056 Human Polypeptide
14 10 100.0 128 22 AAO0559 Human polypeptide
15 10 100.0 137 22 AAU30769 Novel human secret
16 10 100.0 140 22 AAM79550 Human protein SEQ
17 10 100.0 141 18 AAU29718 Haemoglobin beta-(
18 10 100.0 142 22 AAU29784 Novel human secret
19 10 100.0 142 22 AAU29796 Novel human secret
20 10 100.0 143 22 AAU29798 Novel human secret
21 10 100.0 143 22 AAU29847 Novel human secret
22 10 100.0 143 22 AAU29890 Novel human secret
23 10 100.0 143 22 AAU29920 Novel human secret
24 10 100.0 143 22 AAU29929 Novel human secret
25 10 100.0 143 22 AAU29955 Novel human secret
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27 10 100.0 143 22 AAU29977 Novel human secret
28 10 100.0 143 22 AAU30020 Novel human secret
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34 10 100.0 143 22 AAU30099 Novel human secret
35 10 100.0 143 22 AAU30132 Novel human secret
36 10 100.0 143 22 AAU32926 Novel human secret
37 10 100.0 144 13 AAR29611 Novel human secret
38 10 100.0 144 14 AAR39726 HbA McKees Rock
39 10 100.0 144 19 AAW73382 Human haemoglobin
40 10 100.0 145 13 AAR20303 Val(1) to Met, His
41 10 100.0 145 13 AAR20306 Val(1) to Met, His
42 10 100.0 145 13 AAR20306 Met(1), His(2) del
43 10 100.0 145 22 AAU301346 Human Polypeptide
44 10 100.0 146 9 AAB81301 Mutant beta-globin
45 10 100.0 146 11 AAR08115 des-Val beta globi
46 10 100.0 146 13 AAR20302 Asp(4) beta-globin
47 10 100.0 146 13 AAR20304 Asp(5) beta-globin
48 10 100.0 146 13 AAR20307 "HCl Lys(144) to A
49 10 100.0 146 13 AAR20308 Glu(3) beta-globin
50 10 100.0 146 13 AAR20309 Asp(3) beta-globin
51 10 100.0 146 13 AAR20310 Glu(69) beta-globin
52 10 100.0 146 13 AAR20311 Asp(49) beta-globin
53 10 100.0 146 13 AAR20312 Asp(5) beta-globin
54 10 100.0 146 13 AAR20313 Glu(5) beta-globin
55 10 100.0 146 13 AAR20314 Ala(5) beta-globin
56 10 100.0 146 13 AAR20315 Glu(69) beta-globin
57 10 100.0 146 13 AAR20316 Asp(69) beta-globin
58 10 100.0 146 13 AAR20317 Thr(70) beta-globi
59 10 100.0 146 13 AAR20318 Ser(70) beta-globi
60 10 100.0 146 13 AAR20319 Cys(75) beta-globi
61 10 100.0 146 13 AAR2031916 Leu(1) beta-globi
62 10 100.0 146 13 AAR21916 Met(75) beta-globi
63 10 100.0 146 13 AAR21918 Arg(76) beta-globi
64 10 100.0 146 13 AAR21919 His(76) beta-globi
65 10 100.0 146 13 AAR21920 Lys(76) beta-globi
66 10 100.0 146 13 AAR21921 Met(1) beta-globi
67 10 100.0 146 13 AAR21922 Leu(1) human beta-globi
68 10 100.0 146 13 AAR21923 Leu(2) human beta-globi
69 10 100.0 146 13 AAR21924 Tyr(2) human beta-globi
70 10 100.0 146 13 AAR21925 Asp(2) human beta-globi
71 10 100.0 146 13 AAR21926 Met(1), Leu(2) hum
72 10 100.0 146 13 AAR21927 Met(1), Tyr(2) hum
73 10 100.0 146 13 AAR21928 Ileu(1), Leu(2) hum
74 10 100.0 146 13 AAR21929 Ileu(1), Asp(2) hum
75 10 100.0 146 13 AAR21930 Ileu(1), Tyr(2) hum
76 10 100.0 146 13 AAR29609 Mutant human beta-globi
77 10 100.0 146 13 AAR29610 Mutant human beta-globi
78 10 100.0 146 14 AAR30527 Agenogi beta globi
79 10 100.0 146 14 AAR30528 E90G beta globin
80 10 100.0 146 14 AAR30529 Yoshizuka beta globi
81 10 100.0 146 14 AAR30530 Kansas beta globin
82 10 100.0 146 14 AAR30531 Beth israel betaglobi
83 10 100.0 146 14 AAR30532 Root effect beta g
84 10 100.0 146 14 AAR32989 Human beta Haemogl

85 10 100.0 146 14 AAR39716
85 100.0 146 14 Human embryonic ep
87 10 100.0 146 14 Human fetal gamma
87 100.0 146 14 CC be used in gene therapy. This peptide fragment of human haemoglobin
88 10 100.0 146 14 Human adult delta
88 100.0 146 14 CC corresponds to amino acids 32-41 of the mature protein given in
89 10 100.0 146 14 AAR39720
89 100.0 146 14 CC AAR39738.
90 10 100.0 146 14 AAR39721
90 100.0 146 14 HbA Deer Lodge, H
91 10 100.0 146 14 Homo Abruzzo, Homo
92 10 100.0 146 14 Des Val beta globi
93 10 100.0 146 14 Natural beta-globi
94 10 100.0 146 15 Human beta haemogl
95 10 100.0 146 15 Adult human beta-g
96 10 100.0 146 15 AAR44523
97 10 100.0 146 15 AAR44524
98 10 100.0 146 15 AAR44525
99 10 100.0 146 15 AAR44526
100 10 100.0 146 15 AAR44527
Adult human beta-g
Adult human beta-g

CC Sequence 10 AA;
RESULT 1
ID AAR97348 standard; Protein; 10 AA.
XX AC AAR97348;
XX AC
XX DT 17-OCT-1996 (first entry)
DE Peptide fragment of haemoglobin B (Haemorphin 10).
XX haemoglobin; INPROL; stem cell proliferation; B lymphocytes;
KW B cells; chemotherapy; cancer; haematopoietic cells; marrow; blood;
KW myeloproliferative disease; autoimmune disease; adjuvant;
vaccination; immunodepression; gene therapy.
XX Homo sapiens.
XX OS WO9610634-A1.
XX PN
XX PD 11-APR-1996.
XX PP 29-SEP-1995; 95WO-0512268.
XX PR 28-SEP-1995; 95US-0535882.
XX PR 30-SEP-1994; 94US-0316424.
XX PA (PRON-) PRO-NEURON INC.
XX PI Kozlov V, Tsyriova I, Wolpe SD;
XX DR WPI; 1996-209356/21.
XX PS Inhibitors of stem cell proliferation comprising haemoglobin chains
- useful in mammals, e.g. for protecting stem cells from antiviral
agents, treating cancer, and maintaining mammalian haematopoietic
stem cells ex vivo
PS Claim 17; Page 65; 101PP; English.

XX PT The present peptide is derived from amino acids 32-41 of the beta
CC chain of adult human haemoglobin. The peptide has sequence similarity
CC and biological activity similar to other atypical opiate peptides. The
CC peptide can stimulate or inhibit stem cell proliferation, similar to
CC INPROL compounds. The peptide is used to inhibit stem cell proliferation,
CC particularly during radiotherapy or chemotherapy of cancer, but more
CC generally wherever a mammal is exposed to an agent, e.g. an antiviral,
CC that damages or destroys stem cells. It can also be used for differential
CC protection of normal stem cells, but not cancer cells, from chemotherapy
CC or radiation, particularly after normal stem cells have been induced to
CC proliferate by therapeutic treatment. The peptide can also be used for
CC control of stem cell hypoproliferation (e.g. aplastic anaemia), for
CC treating or preventing stem cell exhaustion (e.g. where caused by
CC acquired immune deficiency syndrome), and to treat or prevent
CC immunodeficiency. INPROL can also be used for treating pain in a mammal.
CC INPROL and related compounds reversibly inhibit or stimulate stem cells
depending on the dose, so allow precise control over cycling of these
CC cells.

XX Sequence 10 AA;

XX Query Match, Similarity 100.0%; Score 10; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 1 lvvypwtqrf 10

RESULT 3
AAW37247 standard; peptide; 10 AA.
XX
AC AAW37247;
XX DT 18-JUN-1998 (first entry)
XX DE Angiotensin IV activity exhibiting neuroactive peptide LVV-haemorphin-7.
XX KW Angiotensin IV; neuroactive; Alzheimer's disease; modulator; dementia;
neuronal development; vasoeffective; neuropathy; brain injury;
LVV-haemorphin-7.
XX OS Synthetic.
OS Macaca fascicularis.
PN WO9801465-A1.
XX PD 15-JAN-1998.
XX PF 09-JUL-1997; 97WO-AU00436.
PR 09-JUL-1996; 96AU-0000893.
XX (FLOR-) FLOREY INST EXPERIMENTAL PHYSIOLOGY.
PI Aldred PG, Chai SY, Lew RA, Mendelsohn FAO, Moeller R;
Smith LA;
PR DR 1998-100095/09.

XX Neuro-active peptide with activities of angiotensin IV and related
DNA - antagonists and oligonucleotide(s), useful for modulating
neuronal development and activity of motor and cholinergic neurons
XX
PS Claim 1; Page 45; 65pp; English.

XX This LVV-haemorphin-7 is a neuroactive peptide with at least 1 of the
activities of angiotensin IV. This is an agonist of the angiotensin IV
receptor and is its endogenous ligand in the brain. It can modulate
learning or behaviour and has vasoactive effects and can dilate cerebral
arteries, increase renal blood flow and stereotype behaviour, facilitate
memory retrieval, induce neurite remodelling, and alleviate effects of
spinal cord injuries. This peptide and its antagonists are used to
modulate activity of motor, cholinergic neurons and neuronal development.
CC Specific applications are in treatment of dementia, Alzheimer's disease,
neurodegeneration (involving cholinergic, motor or sensory pathways),
sensory and motor peripheral neuropathy, brain injury and spinal cord
injury (caused by one or more of trauma, hypoxia and/or vascular
disease). Antibodies specific for the peptide can be used to determine
its amount of in tissues and tissue regions.

XX Sequence 10 AA;

XX Query Match, Similarity 100.0%; Score 10; DB 6; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.0001; Mismatches 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 2 lvvypwtqrf 11

RESULT 4
AAAP50291 standard; Protein; 74 AA.
ID AAP50291
XX AC AAP50291;
XX DT 30-NOV-1991 (first entry)
DE Sequence encoded by second exon of rabies glycoprotein gene.
XX Rabies vaccine; therapy; glycoprotein; antigen; diagnosis.
XX OS Rabies virus.
PN WO8901516-A.
XX PD 11-APR-1985.
PF 02-OCT-1984; 84WO-4000217.
XX PR 27-MAR-1984; 84FR-0004754.
PR 03-OCT-1984; 84FR-0015716.
PR 03-OCT-1983; 83FR-0015716.
XX PA (TRAN-) TRANSGENE SA.
PA (LATH/) LATHE R.
XX PI Lathe R, Kiery MP, Lemoine Y, Loison G, Aigle M;
DR N-PDBB; AAN50333.
XX PT WPI; 1985-098445/16.
PT N-PDBB; AAN50333.
XX Example; Fig 10; 62pp; French.
PS The inventors claim a vector for expressing a rabies antigen protein
in eucaryotic cells. After glycosylation with a yeast (specifically
at ASP residues 204 and 319), the recombinant antigen protein is
useful as a vaccine or curative agent. The coding sequence in the
vector can be followed by an intron (see AAN50333, N50334) or sites of
CC polyadenylation.
XX Sequence 74 AA;

RESULT 5
AAR9602 standard; Protein; 74 AA.
ID AAR9602
XX AC AAR9602;
XX DT 25-SEP-1995 (first entry)
XX DE Human beta-globin encoded by optimised exon 2.
XX KW Beta-globin; optimised codons; exon 2.

OS Synthetic.
 XX
 PN WO9504744-A.
 XX
 PD 16-FEB-1995.
 XX
 PF 29-JUL-1994; 94W0-US08630.
 XX
 PR 11-AUG-1993; 93US-0105989.
 XX
 PA (DNXD-) DNX CORP.
 XX
 PT Khoury-christianson AM, Kumar R, Midha S, Paulhac C;
 PI Sharma A;
 XX
 DR WPI: 1995-090838/12.
 N-PSDB; AAQ83723.
 XX
 PT Production of human haemoglobin in transgenic pigs - by introducing gene constructs comprising human alpha and beta globin genes into pig ova, for an efficient source of haemoglobin for use in e.g. transfusions
 PS Example: Fig 39; 15pp; English.
 XX
 CC Human alpha-globin is expressed in transgenic pigs at higher levels than human beta-globin. One approach to increasing the level of expressed beta-globin is to engineer the human beta-globin gene from the promoter region through the coding sequence and into the polyA site and 3' UTR to be similar to pig beta-globin gene, but without altering the AA sequence from that of authentic wt human beta-globin. PCR was used to optimise human beta-globin gene for porcine expression. Equivalent fragments of the human and pig beta-globin coding sequences in exons 1, 2 are 3 are depicted in AAQ83716/083719, AAQ83717/083720 and AAQ83718/083721, respectively. These pairs of sequences may be compared for differences. Optimised human beta-globin coding sequences for exons 1, 2 and 3 are depicted in AAQ83722, AAQ83723 and AAQ83724, respectively. The AA sequences encoded by the optimised human beta-globin coding sequences are given in AAR69601, AAR69602, AAR69603.

SQ Sequence 74 AA;

Query Match	Score	DB	Length	
Best Local Similarity	100.0%	16	74;	
Matches	10;	Conservative	0;	
	Mismatches	0;	Indels	0;
	Gaps	0;		

QY 1 LVVYPWTQRF 10
 AC |||||||
 DB 2 lvvypwtqrf 11

RESULT 6
 AAC07245
 ID AAO07245 standard; Protein; 86 AA.
 XX
 AC AAO07245;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 21137.

XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy; tissue growth factor; immunomodulator; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.

PD 07-SEP-2001.
 XX
 PN 26-FEB-2001; 2001WO-US04927.
 XX
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PT Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI: 2001-514838/56.
 DR N-PSDB; AAI87176.
 XX
 PS Isolated nucleic acids and polypeptides, useful for preventing PT diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
 XX
 PS Claim 20; SEQ ID NO 21137; 139pp + Sequence Listing; English.
 XX
 CC The invention relates to human-polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA00010-AA03910) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity, activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 86 AA;

Query Match	Score	DB	Length	
Best Local Similarity	100.0%	10	86;	
Matches	10;	Conservative	0;	
	Mismatches	0;	Indels	0;
	Gaps	0;		

QY 1 LVVYPWTQRF 10
 AC |||||||
 DB 39 lvvypwtqrf 48

RESULT 7
 AAU30074
 ID AAU30074 standard; Protein; 104 AA.
 XX
 AC AAU30074;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #565.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haemopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PR 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552329.
 PR 26-JAN-2001; 2001US-0577160.
 XX
 PA (HYSE-) HYSEQ INC.

CC treatment in vascular diseases.
 XX
 SQ Sequence 112 AA;

Query Match	Score	DB	Length	Indels	Gaps
Best Local Similarity	100.0%	16	112	0	0
Matches	10;	Conservative	0;	Mismatches	0;
ID	AAR89261	standard; peptide	112 AA.		
AC	AAR89261;				
XX					
DT	04-MAR-1996	(first entry)			
DE	Human beta-globin mutant Gln/Lys90 and Asp108.				
XX					
KW	Human beta-globin; mutant Gln/Lys90 and Asp108; hypoxic cells; increased oxygenation; radiation therapy; vascular diseases.				
XX					
OS	Homo sapiens.				
XX					
FH	Key Location/Qualifiers				
FT	Misc-difference 90 /label= Gln, Lys				
XX					
PN	US5428007-A.				
XX					
PD	27-JUN-1995.				
XX					
PF	06-OCT-1989; 89US-0417949.				
XX					
PR	06-OCT-1989; 89US-0417949.				
XX					
PR	09-OCT-1992; 92US-0959266.				
XX					
PR	28-APR-1994; 94US-0235118.				
XX					
PA	{UYYA } UNIV YALE.				
XX					
PI	Baserga SJ, Fischer JJ;				
XX					
DR	WPI; 1995-240064/31.				
XX					
PT	Increasing tissue oxygen in hypoxic cells - by administering a pure PT mutant alpha or beta haemoglobin having a low oxygen affinity.				
XX					
PS	Example 3; Columns 5-6; 10pp; English.				
XX					
CC	AAR89261 is the human beta-globin mutant Gln/Lys90 and Asp108.				
CC	The mutant globin can be used to increase tissue oxygenation in hypoxic cells, to increase oxygenation in tumours to enhance the effects of radiation therapy or as a blood replacement or treatment in vascular diseases.				
CC					
XX	Sequence 112 AA;				
SQ	Sequence 121 AA;				
RESULT 10					
QY	1 LVVYPWTQRF 10				
Db	32 lvvypwtqrf 41				
Query Match	100.0%	Score	10;	DB	16;
Best Local Similarity	100.0%	Pred. No.	0.00015;	Length	112;
Matches	10;	Conservative	0;	Indels	0;
ID	AAR29698	standard; Protein	124 AA.		
XX					
AC	AAR29698;				
XX					
DT	18-DEC-2001	(first entry)			
XX					
DE	Novel human secreted protein #189.				
XX					
KW	Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration;				

RESULT 12

Query Match	Score	DB	Length	Indels	Gaps
Best Local Similarity	100.0%	21;	121;	0	0
Matches	10;	Conservative	0;	Mismatches	0;
ID	AAU29698	standard; Protein	124 AA.		
XX					
AC	AAU29698;				
XX					
DT	Novel human secreted protein #189.				
XX					
DE	Novel human secreted protein #189.				
XX					
KW	Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration;				

RESULT 11

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 'XX
 PN WO200179449-A2.
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2000US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX
 PS Claim 20; Page 181; 765pp; English.
 XX
 The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate hematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. RAI9510-RAI95304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 SQ Sequence 124 AA;

Query Match 100.0%; Score 10; DB 22; Length 124;
 Best Local Similarity 100.0%; Pred. No. 0.00016; Mismatches 10; Conservative 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||||||
 Db 39 lvvypwtqrf 48

RESULT 13
 AAO13066
 ID AAO13066 standard; Protein: 127 AA.
 XX
 AC AAO13066;
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 26958.

XX
 Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04927.
 XX
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.

PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04927.
 XX
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.

PS Claim 20; SEQ ID NO 26958; 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polyribonucleotides (RAI9941-RAI9541) and
 CC the encoded proteins (AA00010-AA013910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polyribonucleotides and polypeptides are useful in gene therapy, vaccines or
 CC pepipide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haemopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at http://ftp.wipo.int/pub/published_pct-sequences.
 XX
 Sequence 127 AA;

Query Match 100.0%; Score 10; DB 22; Length 127;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 10; Conservative 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||||||
 Db 39 lvvypwtqrf 48

RESULT 14
 AAC09585
 ID AAC09585 standard; Protein: 128 AA.
 AC AAC09585;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 23477.

XX
 Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 OS Homo sapiens.
 XX
 PN WO200164835-A2.

XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04927.
 XX
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.

PA (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-514338/56.
 DR N-PSDB; AAI89316.
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders.
 XX Claim 20: SEQ ID NO 23477; 1399pp + Sequence Listing; English.
 CC The invention relates to human polyribonucleotides (AA17941-AA19381) and
 CC the encoded proteins (AA00010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polyribonucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haemopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity, and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 Note: The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 128 AA;
 Query Match 100.0%; Score 10; DB 22; Length 128;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0;
 Matches 10; Conservative 0; Indels 0; Gaps 0;
 Qy 1 LVVYPPWTQRF 10
 |||||||
 Db 39 Ivvypwtqrf 48
 RESULT 15
 AUU30769 ID AUU30769 standard; Protein; 137 AA.
 XX AC AAU30769;
 XX DT 18-DEC-2001 (first entry)
 DE Novel human secreted protein #1260.
 XX Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 OS Homo sapiens.
 XX WO200179449-A2.
 XX 25-OCT-2001.
 PD 16-APR-2001; 2001WO-US08656.
 XX 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-611725/70.
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 vaccination, testing and therapy -
 PT vaccination, testing and therapy -
 XX
 PS Claim 20; Page 342; 765pp; English.
 XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 The proteins are useful in genetic vaccination, testing and
 therapy, and can be used as nutritional supplements. They may be used to
 increase stem cell proliferation; to regulate haemopoiesis; and in
 bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC sequences of novel human secreted proteins of the invention.
 CC SQ Sequence 137 AA;
 Query Match 100.0%; Score 10; DB 22; Length 137;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0;
 Matches 10; Conservative 0; Indels 0; Gaps 0;
 Qy 1 LVVYPPWTQRF 10
 |||||||
 Db 51 Ivvypwtqrf 60
 RESULT 16
 AUU30769 ID AAM79250 standard; Protein; 140 AA.
 XX AC AAM79250;
 XX DT 06-NOV-2001 (first entry)
 DE Human protein SEQ ID NO 1912.
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; Peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 OS Homo sapiens.
 XX WO200157190-A2.
 XX 09-AUG-2001.
 PD 05-FEB-2001; 2001WO-US04098.
 XX PR 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0653561.
 PR 20-OCT-2000; 2000US-0653325.
 PR 30-NOV-2000; 2000US-0728422.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX DR WPI; 2001-47283/51.
 DR N-PSDB; AAK2383.

XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities,
 useful in diagnosis and gene therapy -
 XX
 PS Claim 20; Page 4310-4311; 6221pp; English.

The invention relates to polynucleotides (AK5456-AK53435) and the encoded polypeptides (AAW7323-AAW8032) that exhibit activity elating to cytokine cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g.: stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activating/inhibiting activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.

Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAW80320) are omitted as the relevant pages from the sequence listing were missing at the time of publication.

SQ Sequence 140 AA:

```
Query Match 100.0%; Score 10; DB 22; Length 140;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 LVVYPWTQRF 10
 Db 33 lvvypwtqrf 42

RESULT 17

ID AAW30718 standard; Protein: 141 AA.

AC AAW30718;

XX

DT 14-JAN-1998 (first entry)

DE Haemoglobin beta(D) variant chain.

XX

KW Haemoglobin; Hb; alpha; beta; wild type; variant; haem loss; stability; red blood cell substitute; volume expander; gss content; drug delivery; imaging; scavange; haemolytic anaemia; porphyria; haemochromatosis.

XX

OS Synthetic.

OS Homo sapiens.

XX

WO715511-A1.

XX

PD 01-MAY-1997.

XX

PF 23-OCT-1996; 96WO-US16934.

XX

PR 23-OCT-1995; 95US-0006020.

PR 04-DEC-1995; 95US-0566780.

PA (RICV) UNIV RICE.

XX

PT Hargrove MS, Olson JS, Whitaker TL;

XX

DR WPI: 1997-258953/23.

XX

PT Reducing haem loss in haemoglobin by specific amino acid alterations - to improve stability and recombinant expression, useful as blood substitutes, scavengers of excess haem etc.

XX

PS Claim 6; Page -; 30pp; English.

XX This is a human haemoglobin (Hb) beta chain variant, designated

CC betal(-D), created by deletion of residues Thr50-Pro-Asp-Ala-Val54 from the native sequence (see AAW0717). Hb variants (AAW7018-30 and AAW7033-36) were used to create single and double mutant Hb hybrids in combination with wild type alpha (AAW30716) and beta chains. Novel mutant Hbs where the substitution is not specified are indicated in AAW30731-32.

CC Other Hb mutants are known. The rate of haemin loss in the Hb mutants was determined by assays for ligand binding, autooxidation rates and haemin dissociation rates. In particular haem loss in Hb is reduced by altering the sequence of a Hb subunit with one of the following mutations: (a) addition of a D-helix region to an alpha subunit; (b) altering Leu8(B10), Met32(B13), Thr8(C4), Phe41(C7), Phe42(CD1), Ser44(CD3), Phe5(CD4), the entire D helix, His63(E7), Gly64(E8), Lys66(E10), Val67(E11), Ala70(E14), Leu80(F4), Leu81(F7), His92(F8), Leu96(FG3), Val98(FG5), Asn102(G4), Phe103(G5), Leu106(G8), Leu110(G12), Gly136(H14), Val137(H15) or Leu141(H19) in the beta subunit; and (c) altering Leu9(B10), Leu31(B13), Thr39(C4), Tyr42(C7), Phe43(CD1), His55(CD3), Phe66(CD4), His58(E7), Glu59(E8), Lys61(E10), Val62(E11), Ala65(E14), Phe68(G5), Leu101(G8), Leu102(G12), Ser131(N14), Val132(H15), or Leu136(H19) in the alpha subunit. The mutant Hb are used as red blood cell substitutes or volume expanders; as reference solutions for analytical instruments; as reagents; to control gas content of cell cultures (delivery or removal of oxygen); for drug delivery and imaging; to remove/deliver nitric oxide or non-oxygen ligands and to scavenge excess haem (e.g. for treatment of haemolytic anaemia, porphyria or haemochromatosis).

CC Sequence 141 AA:

```
Query Match 100.0%; Score 10; DB 18; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 LVVYPWTQRF 10
 Db 32 lvvypwtqrf 41

RESULT 18

ID AAU29784 standard; Protein: 142 AA.

AC AAU29784;

XX

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #275.

XX

KW Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX

OS Homo sapiens.

XX

WO200179449-A2.

XX

PD 25-OCT-2001.

XX

XX

PF 16-APR-2001; 2001WO-US08656.

XX

PN WO200179449-A2.

XX

PR 18-APR-2000; 2000US-0557929.

PR 26-JAN-2001; 2001US-0770160.

PA (HYSE-) HYSEQ INC.

XX

PT Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-611725/70.

XX

PT Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -

XX

PS Claim 20; Page 194; 765pp; English.

XX CC

CC The invention relates to novel human secreted polypeptides. The

CC polypeptides and antibodies to the polypeptides are useful for

CC determining the presence of or predisposition to a disease associated

CC with altered levels of polypeptide. The polypeptides are also useful for

CC identifying agents (agonists and antagonists) that bind to them. Cells

CC expressing the proteins are useful for identifying a therapeutic agent

CC for use in treatment of a pathology related to aberrant expression or

CC physiological interactions of the polypeptide. Vectors comprising

CC the nucleic acids encoding the polypeptides and cells genetically

CC engineered to express them are also useful for producing the proteins.

CC The proteins are useful in genetic vaccination, testing and

CC therapy, and can be used as nutritional supplements. They may be used to

CC increase stem cell proliferation; to regulate haematopoiesis; and in

CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;

CC physiological interactions of the polypeptide. Vectors comprising

CC the nucleic acids encoding the polypeptides and cells genetically

CC engineered to express them are also useful for producing the proteins.

CC The proteins are useful in genetic vaccination, testing and

CC therapy, and can be used as nutritional supplements. They may be used to

CC increase stem cell proliferation; to regulate haematopoiesis; and in

CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;

CC immune suppression and/or stimulation; as anti-inflammatory agents; and

CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid

CC sequences of novel human secreted proteins of the invention.

CC Sequence 142 AA;

Query Match 100.0%; Score 10; DB 22; Length 142;

Best Local Similarity 100.0%; Pred. No. 0.0019; Mismatches 0; Indels 0; Gaps 0; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWQRF 10

Db 28 lvvypwqr 37

RESULT 19

ID AAU29796 standard; Protein: 143 AA.

AC AAU29796;

XX 18-DEC-2001 (first entry)

DE Novel human secreted protein #287.

XX Human; vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

XX WO200179449-A2.

XX 25-OCT-2001.

PD 16-APR-2001; 2001WO-US08656.

XX PR 18-APR-2000; 2000US-0552929.

XX PR 26-JAN-2001; 2001US-0770160.

PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-611725/70.

PR Nucleic acids encoding a range of human polypeptides, useful in genetic

PT vaccination, testing and therapy -

XX PS Claim 20; Page 195; 765pp; English.

XX CC

CC The invention relates to novel human secreted polypeptides. The

CC polypeptides and antibodies to the polypeptides are useful for

CC determining the presence of or predisposition to a disease associated

CC with altered levels of polypeptide. The polypeptides are also useful for

CC identifying agents (agonists and antagonists) that bind to them. Cells

CC expressing the proteins are useful for identifying a therapeutic agent

CC for use in treatment of a pathology related to aberrant expression or

CC physiological interactions of the polypeptide. Vectors comprising

CC the nucleic acids encoding the polypeptides and cells genetically

CC engineered to express them are also useful for producing the proteins.

CC The proteins are useful in genetic vaccination, testing and

CC therapy, and can be used as nutritional supplements. They may be used to

CC increase stem cell proliferation; to regulate haematopoiesis; and in

CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;

CC immune suppression and/or stimulation; as anti-inflammatory agents; and

CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid

CC sequences of novel human secreted proteins of the invention.

Query Match 100.0%; Score 10; DB 22; Length 143;

Best Local Similarity 100.0%; Pred. No. 0.0019; Mismatches 0; Indels 0; Gaps 0; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWQRF 10

Db 29 lvvypwqr 38

RESULT 20

ID AAU29798 standard; Protein: 143 AA.

XX AC AAU29798;

XX 18-DEC-2001 (first entry)

DE Novel human secreted protein #289.

XX Human; vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

XX PN WO200179449-A2.

XX PD 25-OCT-2001.

PR 16-APR-2001; 2001WO-US08656.

XX PR 18-APR-2000; 2000US-0552929.

XX PR 26-JAN-2001; 2001US-0770160.

PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-611725/70.

PR Nucleic acids encoding a range of human polypeptides, useful in genetic

PT vaccination, testing and therapy -

XX PS Claim 20; Page 195; 765pp; English.

XX CC

CC The invention relates to novel human secreted polypeptides. The

CC polypeptides and antibodies to the polypeptides are useful for

CC determining the presence of or predisposition to a disease associated

CC with altered levels of polypeptide. The polypeptides are also useful for

CC identifying agents (agonists and antagonists) that bind to them. Cells

CC expressing the proteins are useful for identifying a therapeutic agent

CC for use in treatment of a pathology related to aberrant expression or

CC physiological interactions of the polypeptide. Vectors comprising

CC the nucleic acids encoding the polypeptides and cells genetically

CC engineered to express them are also useful for producing the proteins.

CC The proteins are useful in genetic vaccination, testing and

CC therapy, and can be used as nutritional supplements. They may be used to

CC increase stem cell proliferation; to regulate haematopoiesis; and in

CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;

CC immune suppression and/or stimulation; as anti-inflammatory agents; and

CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid

CC sequences of novel human secreted proteins of the invention.

increase stem cell proliferation; to regulate haemopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU9510-AAU33304 represent the amino acid sequence of bovine pro-keratinocyte growth factor, and may represent, inc-

CC CC CC CC CC
immune system; bone marrow; cartilage; tendon and/or nerve tissue growth or regeneration; and immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33301 represent the amino acid sequences of novel human secreted proteins of the invention.

```

Query Match          100 %; Score 10; DB 22; Length 143;
Best Local Similarity 100 %; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy   1 lVvypwtqrf 10
      |||||||||
Db   29 lVvypwtqrf 38

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Qry	1	LWVYPTQRF	10		Indels	0	Gaps	0
Dbs	29	lvvypwtqrf	38					

RESULT 22
AAU29890 ID AAU29890 standard; Protein: 143 AA
XX AC AAU29890;
XX

RESULT	21
ID	AAU29847
AAU29847 standard; protein; 143 AA.	
XX	
AC	
AAU29847;	
XX	
DT	18-DESC-2001 (first entry)
XX	
DE	Novel human secreted protein #338.
XX	
XX	Human; vaccination; gene therapy; nutritional supplement;
KW	stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX	
OS	Homo sapiens.
XX	
OS	Homo sapiens.
XX	
XX	Human; vaccination; gene therapy; nutritional supplement;
KW	stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX	
PN	W0200179449-A2.
XX	
PD	25-OCT-2001.
XX	
PR	16-APR-2001; 2001WO-US08656.
XX	
PR	18-APR-2000; 2000US-0552929.
PR	26-JAN-2001; 2001US-0770160.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Liu C, Drmanac RT;
XX	
PI	Tang YT, Liu C, Drmanac RT;
XX	
DR	WPI; 2001-611725/70.
XX	
PT	Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
XX	
PT	Claim 20; Page 207; 765PP; English.
XX	
PS	The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cell expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AU29510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.
SQ	Sequence 143 AA:
Query	1
Match	100.0%
Best Local Similarity	100.0%
Matches	Pred. No. 0.00019;
10;	Mismatches 0;
Conservative	Indels 0;
0;	Gaps 0;
CC	LVYWPWTORF 10

Db 29 ||||||| 1vvypwtqrf 38

RESULT 23
ID AAU29220 standard; Protein: 143 AA.
XX
AC AAU29220;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #411.
XX
KW Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haemopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PR 16-APR-2001; 2001WO-US08656.
XX
PR 18-APR-2000; 2000US-0552929.
PR 26-JAN-2001; 2001US-0770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
XX
PS Claim 20; Page 210; 765pp; English.

The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haemopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and sequences of novel human secreted proteins of the invention.

CC Sequence 143 AA;

Query Match 100.0%; Score 10; DB 22; Length 143; Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 25
ID AAU29255 AAU39055 standard; Protein: 143 AA.
XX
AC AAU29255;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #446.

Db 29 1vvypwtqrf 38

Query Match 100.0%; Score 10; DB 22; Length 143; Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 24
ID AAU29229 standard; Protein: 143 AA.

KW	Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.	XX	
KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia.	XX	
OS	Homo sapiens.	XX	
PN	WO200179449-A2.	XX	
PD	25-OCT-2001.	XX	
XX		XX	
PF	16-APR-2001; 2001WO-US08656.	XX	
XX		XX	
PR	18-APR-2000; 2000US-0552929.	XX	
PR	26-JAN-2001; 2001US-0770160.	XX	
PA	(HYSE-) HYSEQ INC.	XX	
XX		XX	
PT	Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -	PT	
PT	vaccination, testing and therapy -	PT	
PS	Claim 20; Page 213; 765pp; English.	PS	
XX		XX	
DR	WPI; 2001-611725/70.	DR	
XX		XX	
PT	Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -	PT	
PT	vaccination, testing and therapy -	PT	
XX		XX	
XX		XX	
CC	The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.	CC	
CC	The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.	CC	
CC	The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.	CC	
SQ	Sequence 143 AA;	SQ	
Query Match	100.0%; Score 10; DB 22; Length 143;	Query Match	100.0%; Score 10; DB 22; Length 143;
Best Local Similarity	100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity	100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 LVVVPPWTQRF 10	Qy	1 LVVVPPWTQRF 10
AC		AC	
Db	29 lvvypwtqrf 38	Db	29 lvvypwtqrf 38
RESULT	26	RESULT	27
AAU29961	ID AAU29961 standard; Protein; 143 AA.	AAU29977	ID AAU29977 standard; Protein; 143 AA.
AC	AAU29961;	AC	AAU29977;
XX		XX	
DE	Novel human secreted protein #452.	DE	Novel human secreted protein #468.
XX		XX	
KW	Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.	KW	Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia.	KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia.
OS	Homo sapiens.	OS	Homo sapiens.
PN	WO200179449-A2.	PN	WO200179449-A2.
XX		XX	
PD	25-OCT-2001.	PD	25-OCT-2001.
XX		XX	
PF	16-APR-2001; 2001WO-US08656.	PF	16-APR-2001; 2001WO-US08656.
XX		XX	
PR	18-APR-2000; 2000US-0552929.	PR	18-APR-2000; 2000US-0552929.
XX		XX	
OS	Homo sapiens.	OS	Homo sapiens.
PN	WO200179449-A2.	PN	WO200179449-A2.

XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.

XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
 XX
 PS Claim 20; Page 221; 765pp; English.

XX
 CC The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haemopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.

XX
 SQ Sequence 143 AA;

Query Match 100.0%; Score 10; DB 22; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 ||||| |||||
 Db 29 lvvypwtqrf 38

RESULT 28
 AAU30020
 ID AAU30020 standard; Protein; 143 AA.
 XX
 AC AAU30020;
 XX
 DT 18-DEC-2001 (first entry)

XX
 DE Novel human secreted protein #511.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haemopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.

XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
 XX
 PS Claim 20; Page 222; 765pp; English.

XX
 CC The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for

PT Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
 XX
 PS Claim 20; Page 221; 765pp; English.

XX
 CC The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haemopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of Leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.

XX
 SQ Sequence 143 AA;

Query Match 100.0%; Score 10; DB 22; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 ||||| |||||
 Db 29 lvvypwtqrf 38

RESULT 29
 AAU30022
 ID AAU30022 standard; Protein; 143 AA.
 XX
 AC AAU30022;
 XX
 DT 18-DEC-2001 (first entry)

XX
 DE Novel human secreted protein #513.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haemopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.

XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
 XX
 PS Claim 20; Page 222; 765pp; English.

XX
 CC The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for

CC determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of Leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.

CC Sequence 143 AA;

CC Query Match Similarity 100.0%; Score 10; DB 22; Length 143; Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 LVVYPTQRF 10

CC Db 29 lvvypwtqrf 38.

RESULT 30

ID AAU30024

ID AAU30024 standard; Protein: 143 AA.

XX AC AAU30024;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secreted protein #515.

XX KW Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX OS Homo sapiens.

XX PN WO200179449-A2.

XX PR 25-OCT-2001.

XX PD 16-APR-2001; 2001WO-US08656.

XX PF 18-APR-2000; 2000US-0552929.

XX PR 26-JAN-2001; 2001US-0770160.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-611725/70.

XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -

XX PS Claim 20; Page 222; 765pp; English.

XX CC The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.

CC Sequence 143 AA;

CC Query Match Similarity 100.0%; Score 10; DB 22; Length 143; Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 LVVYPTQRF 10

CC Db 29 lvvypwtqrf 38.

RESULT 31

ID AAU30028

ID AAU30028 standard; Protein: 143 AA.

XX AC AAU30028;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secreted protein #519.

XX KW Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX OS Homo sapiens.

XX PN WO200179449-A2.

XX PD 25-OCT-2001.

XX PF 16-APR-2001; 2001WO-US08656.

XX PR 18-APR-2000; 2000US-0552929.

XX PR 26-JAN-2001; 2001US-0770160.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-611725/70.

XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -

XX PS Claim 20; Page 222; 765pp; English.

XX CC The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.

CC Sequence 143 AA;

CC Query Match Similarity 100.0%; Score 10; DB 22; Length 143; Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 LVVYPTQRF 10

CC Db 29 lvvypwtqrf 38.

RESULT 31

ID AAU30028

ID AAU30028 standard; Protein: 143 AA.

XX AC AAU30028;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secreted protein #519.

XX KW Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX OS Homo sapiens.

XX PN WO200179449-A2.

XX PD 25-OCT-2001.

XX PF 16-APR-2001; 2001WO-US08656.

XX PR 18-APR-2000; 2000US-0552929.

XX PR 26-JAN-2001; 2001US-0770160.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-611725/70.

XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -

XX PS Claim 20; Page 222; 765pp; English.

XX CC The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.

RESULT 34
 AAU30099
 ID AAU30099 standard; Protein; 143 AA.
 XX
 AC
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #590.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PT (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 CC Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX
 PS Claim 20; Page 239-240; 765pp; English.
 XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC vaccination, testing and therapy -
 XX
 PS Claim 20; Page 239-240; 765pp; English.
 XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation, to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX
 SQ Sequence 143 AA;
 Query Match 100.0%; Score 10; DB 22; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.0001; Mismatches 0;
 Matches 10; Conservative 0; Indels 0; Gaps 0;
 RESULT 35
 QY 1 LVVYPWTQRF 10
 ID AAU30132 standard; Protein; 143 AA.
 XX
 Db 29 lvvypwtqrf 38
 RESULT 35
 ID AAU30132 standard; Protein; 143 AA.
 XX
 AC
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #3417.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 DT 18-DEC-2001 (first entry)

Page 19

xx
DR WPT: 1993-167394/20

WBT: 1993-167394/30

New haemoglobin variants bind reversibly to oxygen - useful as physiological oxygen carriers (e.g. in blood substitutes) and as

Disclosure: Page 13: 211PP; English.

www.IBM.com

This sequence represents a human haemoglobin beta chain variant. DNA encoding this sequence is used in the recombinant DNA vector of the invention, which expresses a globin chain in a yeast cell, and comprises:

- (a) a first DNA sequence encoding a globin chain;
- (b) a yeast transcriptional promoter which promotes the transcription of the first DNA sequence;
- (c) a second DNA sequence encoding a yeast selectable marker; and
- (d) a yeast replication origin.

The vectors and recombinant yeast cells containing them can be used for the recombinant production of the globin chains and their variants. The products in turn, can be used as substitute blood products, where oxygen carriage is required. The variants are designed to enable generally stable cross-linking of monomers to a tetrameric form, which does not dissociate into dimers. They are also designed to be stable to a certain extent in alkaline conditions compared to normal physiological conditions. The yeast strains used allow recombinant production of correctly processed haemoglobin chains in large quantities. The use of recombinant blood also eliminates risks of contamination of donated blood samples, and also shortages of not having enough donations of a specific blood type.

N.B. This sequence was created from the human haemoglobin beta chain sequence given in the specification.

```

Query Match          100.0%; Score 10; DB 14; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy   1  lVvYpWtQRF 10
     ||||| |
Db   32  lVvYpWtQRF 41

```

```

Query Match          100.0%; Score 10; DB 19; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0;
Qy   1 LWWFWWTQRF 10
      ||||||||| 0
Db   32 LWWFWWTQRF 41

```

RESULT	39
AAW73382	standard; protein; 144 AA.
ID	AAW73382
XX	
AC	
AAW73382;	
XX	
DT	18-FEB-1999 (first entry)
XX	
DE	Human haemoglobin beta-chain mutant Y115Stop.
XX	
KW	Haemoglobin; mutant; human; substitute blood product; synthetic blood beta chain.
XX	
OS	Homo sapiens.
XX	
PN	US5827693-A.
XX	
PF	07-JUN-1995; 95US-0484686.
XX	
PD	27-CCT-1998.
XX	
PF	29-APR-1992; 92US-0874290.
PR	16-NOV-1990; 90US-050918.
PR	14-NOV-1990; 90US-0614359.
PR	12-APR-1991; 91US-0684611.
PR	29-DEC-1994; 94US-036407.
PR	07-JUN-1995; 95US-0484686.
XX	
PA	(APEX-) APEX BIOSCIENCE INC.
XX	
PI	Bajwa W, Bonaventura J, De Angelo J, Motwani NN;
XX	
DR	WPT; 1998-593993/50.
XX	
PT	Recombinant expression of globin chains - and variants in yeast, useful as substitutes for natural blood required for oxygen carriage
XX	
PS	Claim 54; Page - ; 144pp; English.
XX	

AAR20303
ID AAR20303 standard; Protein; 145 AA.
XX
AC AAR20303;
XX
XX
DT 13-APR-1992 (first entry)
XX
DE Val(1) to Met, His(2) deleted beta-globin mutant.
XX
KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb.
XX
OS Homo sapiens.
XX
PN WO9119505-A.
XX
PD 26-DEC-1991.
XX
PP 20-JUN-1991; 91WO-US041156.
XX
PR 20-JUN-1990; 90US-0541011.
XX
PA (RESE-) RES CORP TECHN INC.
XX
PI Fronticelli C, Bucci E, Brinigar W;
XX
DR
WPI; 1992-024191/03.
XX
PT Modified beta-chain of human haemoglobin - with aminoacid changes
PT to reduce oxygen affinity, used in blood prods. for transfusion,
PT with enhanced chloride sensitivity
XX
PS Claim 5; Page 60; 87pp; English.
XX
CC The modified beta-globin chain differs from the wild-type protein
CC sequence in that it has Val at position 1 replaced by Met and His
CC at position 2 deleted. It is one of the preferred mutant proteins
CC covered by the invention having reduced oxygen affinity compared
CC to wild-type beta-chain. See also AAQ20236-8 and AAR20300-R20317.
XX

SQ sequence: 145 AA;

Query Match 100.0%; Score 10; DB 13; Length 145;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTQRF 10
 |||||||||
 Db 31 lvvypwtqrf 40

RESULT 41

AARR20305 41
 ID AAR20305 standard; Protein: 145 AA.

XX
 DE Met(1), His(2) deleted, Lys(76), Arg(144) beta-globin mutant.
 XX
 KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KW NAL (1) Val to Met; NAL (2) HIS deleted; E20 (76) Ala to Lys;
 KW HCL (144) Lys to Arg.

XX
 AC Homo sapiens.

XX
 PN WO9119505-A.

PD 26-DEC-1991.

XX
 PR 20-JUN-1991; 91WO-US04156.

XX
 PR 20-JUN-1990; 90US-0541011.

XX
 PA (RESE) RES CORP TECHN INC.

XX
 PI Fronticelli C, Bucci E, Brinigar W;

XX
 DR WO9119505-A.

PD 26-DEC-1991.

XX
 PN WO9119505-A.

XX
 PR 20-JUN-1991; 91WO-US04156.

XX
 PR 20-JUN-1990; 90US-0541011.

XX
 PA (RESE) RES CORP TECHN INC.

XX
 PI Fronticelli C, Bucci E, Brinigar W;

XX
 DR WPI; 1992-024191/03.

XX
 PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity

XX
 PS Claim 9; Page 61; 87pp; English.

XX
 CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Val at position 1 replaced by Met, His
 CC at position 2 deleted, Ala at position 76 replaced by Lys and Lys
 CC at position 144 replaced by Arg. It is one of the preferred mutant
 CC proteins covered by the invention having reduced oxygen affinity
 CC compared to wild-type beta-chain.
 CC See also AAO20336-8 and AAR20300-R20317.

XX
 SQ Sequence 145 AA;

Query Match 100.0%; Score 10; DB 13; Length 145;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTQRF 10
 |||||||||
 Db 31 lvvypwtqrf 40

RESULT 43

AAO10346 43
 ID AAO10346 standard; Protein: 145 AA.

XX
 AC AAO10346;

XX
 DT 06-Nov-2001 (first entry)

XX
 DE Human polypeptide SEQ ID NO 24238.

XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulator; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX
 OS Homo sapiens.

XX
 PN WO200164835-A2.

XX
 PR 07-SEP-2001.

XX
 PR 26-FEB-2001; 2001WO-US04927.

XX
 PR 28-FEB-2000; 2000US-0515126.

RESULT 42

AAR20306 42
 ID AAR20306 standard; Protein: 145 AA.

XX
 AC AAR20306;

XX
 DT 13-APR-1992 (first entry)

PR PR
 XX 16-MAY-2000; 2000US0577409.
 PA (HYSE-) HYSEQ INC.
 XX (SOMA-) SOMATOGENICS (MEDI-) MEDICAL RESEARCH COUNCIL.
 PI Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-514838/56.
 DR N-PSDB; AA190277.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX
 PS Claim 20; SEQ ID NO 24238; 1399pp + Sequence Listing: English.
 XX The invention relates to human polynucleotides (AAI9941-AAI93941) and
 CC the encoded proteins (AA00010-AA013910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haemopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibitory activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 145 AA:
 QY 1 LVVYPWTQRF 10
 ||||| |
 Db 39 lvvypwtqrf 48
 YY
 RESULT 44
 AAP81301
 ID AAP81301 standard; protein; 146 AA.
 XX
 AC AAB81301;
 XX
 DT 16-SEP-1990 (first entry)
 XX
 DE Mutant beta-globin sequence.
 XX
 KW Mutant beta-globin; artificial haemoglobin.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 102..102
 FT /label="Substituted amino acid
 FT /note="Res of known sequence replaced by Thr"
 FT Misc-difference 63..63
 FT /label="Substituted amino acid
 FT /note="Res of known sequence replaced by Phe"
 FT Misc-difference 67..67
 FT /label="Substituted amino acid
 FT /note="Val of known sequence replaced by Ile"
 XX WO8809179-A.
 XX 01-DEC-1988.
 XX
 PF 13-MAY-1988; 88WO-US01534.
 XX
 PR PR
 PA (SOMA-) SOMATOGENICS (MEDI-) MEDICAL RESEARCH COUNCIL.
 XX
 PI Hoffman SJ, Nagai K;
 XX WPI; 1988-353805/49.
 DR N-PSDB; AAN80526.
 XX
 PT Recombinant mutant and artificial haemoglobin - used as blood substitutes
 PT and for altering oxygen concns. in cell cultures or fluids.
 XX
 PS Disclosure: ; 71pp; English.
 XX The sequence is a mutant of beta-globin. The mutant contains only
 CC one of the three possible amino acid changes shown. It is expressed as a
 CC fusion protein with the alpha globin sequence and a spacer peptide,
 CC which is cleaved with Factor Xa. Liberated alpha-globin is
 CC combined with beta-globin from a non-blood source and a source of
 CC haem to form synthetic haemoglobin. This is used in blood
 CC substitute solns. and mutant haemoglobins, whether of reduced or
 CC enhanced oxygen affinity, may be of value for altering oxygen
 CC concns. in cell cultures or extracting oxygen from fluids.
 XX SQ Sequence 146 AA:
 QY 1 LVVYPWTQRF 10
 ||||| |
 Db 32 lvvypwtqrf 41
 YY
 RESULT 45
 AAR08115
 ID AAR08115 standard; protein; 146 AA.
 XX
 AC AAR08115;
 XX
 DT 27-FEB-1991 (first entry)
 XX
 DE des-Val beta globin polypeptide.
 XX
 KW Polycistronic operon; di-alpha-globin; di-beta globin; haemoglobin;
 XX
 OS synthetic.
 XX
 PN WO9013645-A.
 XX
 PD 15-NOV-1990.
 XX
 PP 10-MAY-1990; 90WO-US02654.
 XX
 PR 13-JUL-1999; 89US-0379116.
 PR 10-MAY-1999; 89US-0349623.
 PR 30-JUN-1999; 89US-0374161.
 XX
 PA (SOMA-) SOMATOGENETICS INT.
 XX
 PI Hoffman SJ, Looker DL, Rosenthal MS, Stettler GL, Wagenbach M;
 XX
 DR WPI; 1990-351480/48.
 DR N-PSDB; AAQ06685.
 XX
 PT Di-alpha and di-beta globin-like polypeptides(s) - used for prodn.
 PT of haemoglobin having increased half-life and produced in
 XX
 PT bacteria and yeast
 XX
 PS Disclosure; fig 12; 22pp; English.

CC this beta globin polypeptide is encoded by one cistron of a poly-
 CC cistron operon. It is expressed after the di-alpha polypeptide
 CC as the latter affects folding of the beta globin. This is essential-
 CC for incorporation of the haem molecule to form functional
 CC haemoglobin. The synthetic haemoglobin produced on expression in
 CC a recombinant host, e.g. yeast, cell has an increased intravascular
 CC half life. See also AAQ06684.
 XX Sequence 146 AA;

Query Match 100.0%; Score 10; DB 11; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTFORF 10
 Db 32 lvvypwtqrf 41

RESULT 46
 AAR20302 ID AAR20302 standard; Protein: 146 AA.

XX AC AAR20302;
 XX DT 13-APR-1992 (first entry)
 DE Mutant "E11 (67) Val to Thr" beta-globin.

XX KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb.

XX OS Homo sapiens.

XX PN WO9119505-A.

XX PD 26-DEC-1991.

XX PP 20-JUN-1991; 91WO-US04156.

XX PR 20-JUN-1990; 90US-0541011.

XX PA (RESE) RES CORP TECHN INC.

XX PI FRONTELLI C, BUCCI E, BRINIGAR W;

XX DR WPI; 1992-024191/03.

XX PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity

XX PS Claim 6; Page 60; 87pp; English.

XX CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Lys at position 144 replaced by Arg. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ02036-8 and AAR20300-R20317.

XX SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTFORF 10
 Db 32 lvvypwtqrf 41

RESULT 48
 AAR20307 ID AAR20307 standard; Protein: 146 AA.

XX AC AAR20307;

XX DT 13-APR-1992 (first entry)

DE Glu(3) beta-globin mutant.

XX KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;

XX NA3 (3) Leu to Glu.

XX OS Homo sapiens.

XX PN WO9119505-A.

XX PD 26-DEC-1991.

XX PR 20-JUN-1991; 91WO-US04156.

XX PR 20-JUN-1990; 90US-0541011.

XX RESULT 47
 AAR20304

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTFORF 10
 Db 32 lvvypwtqrf 41

RESULT 48
 AAR20307 standard; Protein: 146 AA.

XX AC AAR20307;

XX DT 13-APR-1992 (first entry)

DE Glu(3) beta-globin mutant.

XX KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;

XX NA3 (3) Leu to Glu.

XX OS Homo sapiens.

XX PN WO9119505-A.

XX PD 26-DEC-1991.

XX PR 20-JUN-1991; 91WO-US04156.

XX PR 20-JUN-1990; 90US-0541011.

PA (RESE) RES CORP TECHN INC.
 XX
 PT Fronticelli C, Bucci E, Brinigar W;
 XX DR WPI; 1992-024191/03.
 PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 XX
 PS Claim 10; Page 62; 87pp; English.
 XX
 CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Leu at position 3 replaced by Glu. It is
 one of the preferred mutant proteins covered by the invention having
 reduced oxygen affinity compared to wild-type beta-chain.
 See also AAQ20236-8 and AAR20300-R20317.

SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0;
 Matches 10; Conservative 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 32 lvvypwtqrf 41

RESULT 50
 AAR20309
 ID AAR20309 standard; Protein; 146 AA.
 XX
 AC AAR20309;
 XX DT 13-APR-1992 (first entry)
 XX DE Glu(4) beta-globin mutant.
 XX KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KW AI (4) Thr to Glu.
 XX OS Homo sapiens.
 XX PN WO9119505-A.
 XX PD 26-DEC-1991.
 XX PR 20-JUN-1991; 91WO-US04156.
 XX PR 20-JUN-1990; 90US-0541011.
 XX PA (RESE) RES CORP TECHN INC.
 XX PI Fronticelli C, Bucci E, Brinigar W;
 XX DR WPI; 1992-024191/03.
 PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 XX
 PS Claim 11; Page 62; 87pp; English.

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0;
 Matches 10; Conservative 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 32 lvvypwtqrf 41

RESULT 51
 AAR20310
 ID AAR20310 standard; Protein; 146 AA.
 XX
 AC AAR20310;
 XX DT 13-APR-1992 (first entry)
 XX DE Asp(4) beta-globin mutant.

XX
 PT Fronticelli C, Bucci E, Brinigar W;
 XX DR WPI; 1992-024191/03.
 PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 XX
 PS Claim 10; Page 62; 87pp; English.
 XX
 CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Leu at position 3 replaced by Asp. It is
 one of the preferred mutant proteins covered by the invention having
 reduced oxygen affinity compared to wild-type beta-chain.
 See also AAQ20236-8 and AAR20300-R20317.

SQ Sequence 146 AA;

KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KW Al (4) Thr to Asp.
 XX PT
 OS Homo sapiens.
 XX PN WO9119505-A.
 XX PD 26-DEC-1991.
 XX PF 20-JUN-1991; 91WO-US04156.
 XX PR 20-JUN-1990; 90US-0541011.
 XX PA (RESE) RES CORP TECHN INC.
 XX PI Fronticelli C, Bucci E, Brinigar W;
 XX WPI; 1992-024191/03.
 XX PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 XX PS Claim 12; Page 62; 87pp; English.
 XX CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Pro at position 5 replaced by Asp. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8 and AAR20300-R20317.
 XX SQ Sequence 146 AA;

XX The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Thr at position 4 replaced by Asp. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8 and AAR20300-R20317.

PS Claim 11; Page 62; 87pp; English.

XX Best Local Similarity 100.0%; Pred. No. 0.00019; Length 146;
 CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC Qy 1 LVVYPWTQRF 10
 CC |||||||
 CC Db 32 lvvypwtqrf 41

XX RESULT 53
 ID AAR20312
 ID AAR20312 standard; Protein; 146 AA.
 XX AC AAR20312;
 XX DT 13-APR-1992 (first entry)
 DE Glu(5) beta-globin mutant.
 XX autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KW A2 (5) Pro to Glu.
 XX OS Homo sapiens.
 XX PN WO9119505-A.
 XX PD 26-DEC-1991.
 XX PF 20-JUN-1991; 91WO-US04156.
 XX PR 20-JUN-1990; 90US-0541011.
 XX PA (RESE) RES CORP TECHN INC.
 XX PI Fronticelli C, Bucci E, Brinigar W;
 XX DR WPI; 1992-024191/03.
 XX PS Claim 12; Page 62; 87pp; English.
 XX CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Pro at position 5 replaced by Glu. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8 and AAR20300-R20317.

XX SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Length 146;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVYPWTQRF 10

XX Modified beta-chain of human haemoglobin - with aminoacid changes

Db 32 lvvypwtqrf 41

RESULT 54
 AAR20313 ID AAR20313 standard; Protein: 146 AA.
 AC AAR20313;
 DT 13-APR-1992 (first entry)
 XX DE Gly(5) beta-globin mutant.
 XX KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KW A2 (5) Pro to Gly.
 XX OS Homo sapiens.
 XX PN WO9119505-A.
 XX PD 26-DEC-1991.
 XX PF 20-JUN-1991; 91WO-US04156.
 PR 20-JUN-1990; 90US-0541011.

(RESE) RES CORP TECHN INC.
 PA Fronticelli C, Bucci E, Brinigar W;
 PI XX DR WPI: 1992-024191/03.

XX PS Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 XX PS Claim 13; Page 62; 87pp; English.
 XX PA Sequence 146 AA;

XX PT Fronticelli C, Bucci E, Brinigar W;
 DR WPI; 1992-024191/03.

XX CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Pro at position 5 replaced by Ala. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 See also AAQ20236-8 and AAR20300-R20317.

XX SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; AC AAR20315;
 QY 1 LVVYPWTQRF 10
 DB 32 lvvypwtqrf 41

RESULT 56
 AAR20315 ID AAR20315 standard; Protein: 146 AA.
 AC AAR20315;
 DT 13-APR-1992 (first entry)
 XX DE Glu(69) beta-globin mutant.
 XX KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KW EL3 (69) GLY to Glu.
 XX OS Homo sapiens.
 XX PN WO9119505-A.
 XX PD 26-DEC-1991.
 XX PF 20-JUN-1991; 91WO-US04156.
 XX PR 20-JUN-1990; 90US-0541011.

(RESE) RES CORP TECHN INC.
 PA Fronticelli C, Bucci E, Brinigar W;
 PI XX DR WPI: 1992-024191/03.

XX CC Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 XX PS Claim 14; Page 62; 87pp; English.
 XX CC The modified beta-globin chain differs from the wild-type protein
 sequence in that it has GLY at position 69 replaced by Glu. It is

RESULT 55
 AAR20314 ID AAR20314 standard; Protein: 146 AA.
 AC AAR20314;
 XX DT 13-APR-1992 (first entry)
 XX DE Ala(5) beta-globin mutant.
 XX KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KW A2 (5) Pro to Ala.
 XX OS Homo sapiens.
 XX PN WO9119505-A.

CC one of the preferred mutant proteins covered by the invention having reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8 and AAR20300-R20317.

XX

SQ Sequence 146 AA;

RESULT 57

AARR20316 Query Match 100.0%; Score 10; DB 13; Length 146;
 ID Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID Db 32 1lvvypwtqrf 41

AC AAR20317;

XX DT 13-APR-1992 (first entry)

XX DE Thr(70) beta-globin mutant.

XX KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb; E14 (70) Ala to Thr.

XX OS Homo sapiens.

XX PN WO9119505-A.

XX PD 26-DEC-1991.

XX PR 20-JUN-1991; 91WO-US04156.

XX PF 20-JUN-1990; 90US-0541011.

XX PR 20-JUN-1991; 90US-0541011.

XX PA (RESE) RES CORP TECHN INC.

XX PI Fronticelli C, Bucci E, Brinigar W;

XX DR WPI; 1992-024191/03.

XX PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity

XX PS Claim 15; Page 63; 87pp; English.

XX CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Ala at position 70 replaced by Thr. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8 and AAR20300-R20317.

XX SQ Sequence 146 AA;

PS

XX PR 20-JUN-1990; 90US-0541011.

XX PA (RESE) RES CORP TECHN INC.

XX PI Fronticelli C, Bucci E, Brinigar W;

XX DR WPI; 1992-024191/03.

XX PS Claim 14; Page 62; 87pp; English.

XX PR Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity

XX SQ Sequence 146 AA;

PS

XX PR 20-JUN-1990; 90US-0541011.

XX PA (RESE) RES CORP TECHN INC.

XX PR 20-JUN-1990; 90US-0541011.

XX PA (RESE) RES CORP TECHN INC.

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 1LVVYPWTQRF 10
 |||||||||
 DB 32 1vvypwtqrf 41

AC AARR21914

XX ID AARR21914 standard; Protein; 146 AA.

AC AARR21914;

XX DT 13-APR-1992 (first entry)

XX DE Ser(70) beta-globin mutant.

XX KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb; E14 (70) Ala to Ser.

XX OS Homo sapiens.

XX PN WO9119505-A.

XX PD 26-DEC-1991.

XX PR 20-JUN-1991; 91WO-US04156.

XX PR 20-JUN-1990; 90US-0541011.

XX PA (RESE) RES CORP TECHN INC.

RESULT 58

AAR20317 Query Match 100.0%; Score 10; DB 13; Length 146;
 ID Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

XX Fronticelli C, Bucci E, Brinigar W;
 PI XX
 XX DR WPI; 1992-024191/03.

XX PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity

XX Claim 15; Page 63; 87pp; English.

CC The modified beta-globin chain differs from the wild-type protein
 sequence in that it has Ala at position 70 replaced by Ser. It is
 one of the preferred mutant proteins covered by the invention having
 reduced oxygen affinity compared to wild-type beta-chain.
 See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.

XX Sequence 146 AA;

Query Match	Score	DB	Length	Indels	Gaps
Best Local Similarity	100.0%	13	146	0	0
Matches	10;	Conservative	0;	Mismatches	0;
Qy	1	LAVVPPWTQRF 10			
Db	32	lvvypwtqrf 41			

RESULT 61
 AAR21916 standard; Protein: 146 AA.

ID AAR21916
 XX AC AAR21916;
 XX DT 13-APR-1992 (first entry)
 XX DE Met(75) beta-globin mutant.
 XX KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KW E19 (75) Leu to Met.
 XX OS Homo sapiens.
 XX PN WO9119505-A.
 XX PD 26-DEC-1991.
 XX PP 20-JUN-1991; 91WO-US04156.
 XX PR 20-JUN-1990; 90US-0541011.
 XX PA (RESE) RES CORP TECHN INC.
 XX PI Fronticelli C, Bucci E, Brinigar W;
 XX DR WPI; 1992-024191/03.

XX PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity

XX PS Claim 16; Page 63; 87pp; English.

CC The modified beta-globin chain differs from the wild-type protein
 sequence in that it has Leu at position 75 replaced by Met. It is
 one of the preferred mutant proteins covered by the invention having
 reduced oxygen affinity compared to wild-type beta-chain.
 See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.

XX Sequence 146 AA;

Query Match	Score	DB	Length	Indels	Gaps
Best Local Similarity	100.0%	13	146	0	0
Matches	10;	Conservative	0;	Mismatches	0;
Qy	1	LAVVPPWTQRF 10			
Db	32	lvvypwtqrf 41			

RESULT 62
 AAR21917 standard; Protein: 146 AA.

ID AAR21917
 XX AC AAR21917;
 XX DT 13-APR-1992 (first entry)
 XX DE Arg(76) beta-globin mutant.
 XX KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;

The modified beta-globin chain differs from the wild-type protein
 sequence in that it has Leu at position 75 replaced by Cys. It is
 one of the preferred mutant proteins covered by the invention having
 reduced oxygen affinity compared to wild-type beta-chain.
 See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.

SQ Sequence 146 AA;

KW E20 (76) Ala to Arg.
 PT with enhanced chloride sensitivity
 XX OS Homo sapiens.
 XX PS Claim 17; Page 63; 87pp; English.
 XX WO9119505-A.
 PN The modified beta-globin chain differs from the wild-type protein
 XX sequence in that it has Ala at position 76 replaced by His. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.
 XX SQ Sequence 146 AA;
 XX PI Fronticelli C, Bucci E, Brinigar W;
 XX WPT; 1992-024191/03.
 XX PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 XX PS Claim 17; Page 63; 87pp; English.
 XX The modified beta-globin chain differs from the wild-type protein
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.
 XX SQ Sequence 146 AA;
 XX Query Match 100.0%; Score 10; DB 13; Length 146;
 CC Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0;
 CC Matches 10; Conservative 0; Indels 0; Gaps 0;
 CC QY 1 LVVYPWTQRF 10
 DB 32 Lvvyypwtqr 41
 XX RESULT 64
 ID AAR21919
 ID AAR21919 standard; Protein; 146 AA.
 XX AC AAR21919;
 XX DT 13-APR-1992 (first entry)
 XX DE Lys(76) beta-globin mutant.
 XX KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KW E20 (76) Ala to Lys.
 XX OS Homo sapiens.
 XX PN WO9119505-A.
 XX PD 26-DEC-1991.
 XX PR 20-JUN-1990; 91WO-US04156.
 XX DE HIS(76) beta-globin mutant.
 XX KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KW E20 (76) Ala to His.
 XX OS Homo sapiens.
 XX WO9119505-A.
 PN The modified beta-globin chain differs from the wild-type protein
 XX sequence in that it has Ala at position 76 replaced by Lys. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.
 XX SQ Sequence 146 AA;
 XX PS Claim 17; Page 63; 87pp; English.
 XX PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 XX PS Claim 17; Page 63; 87pp; English.
 XX The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Ala at position 76 replaced by Lys. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.
 XX SQ Sequence 146 AA;
 XX Query Match 100.0%; Score 10; DB 13; Length 146;
 CC Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0;
 CC Matches 10; Conservative 0; Indels 0; Gaps 0;
 CC QY 1 LVVYPWTQRF 10
 DB 32 Lvvyypwtqr 41

RESULT 65
XX AAR21920
ID AAR21920 standard; Protein: 146 AA.
XX AAR21920;
AC 13-APR-1992 (first entry)
XX DE Met(1) beta-globin mutant.
XX KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
KW NAL (1) Val to Met.
XX OS Homo sapiens.
XX PN WO9119505-A.
XX PR 26-DEC-1991.
XX PF 20-JUN-1991; 91WO-US04156.
XX DR WPI; 1992-024191/03.
XX PT Modified beta-chain of human haemoglobin - with aminoacid changes
PT to reduce oxygen affinity, used in blood prods. for transfusion,
PT with enhanced chloride sensitivity
XX PS Claim 18; Page 63; 87pp; English.
XX PA (RESE) RES CORP TECHN INC.
XX PI Fronticelli C, Bucci E, Brinigar W;
XX DR WPI; 1992-024191/03.
XX CC The modified beta-globin chain differs from the wild-type protein
CC sequence in that it has Val at position 1 replaced by Ieu. It is
CC one of the preferred mutant proteins covered by the invention having
CC reduced oxygen affinity compared to wild-type beta-chain.
CC See also AQQ20236-8, AAR20300-R20317 and AAR21914-R21930.
XX SQ Sequence 146 AA;
XX PS Claim 18; Page 63; 87pp; English.
CC The modified beta-globin chain differs from the wild-type protein
CC sequence in that it has Val at position 1 replaced by Met. It is
CC one of the preferred mutant proteins covered by the invention having
CC reduced oxygen affinity compared to wild-type beta-chain.
CC See also AQQ20236-8, AAR20300-R20317 and AAR21914-R21930.
XX SQ Sequence 146 AA;
Query Match 100.0%; Score 10; DB 13; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0;
Matches 10; Conservative 0; Indels 0; Gaps 0;
QY 1 LVVYPWTQRF 10
||| | | | | |
Db 32 lvvypwtqrf 41
RESULT 67
XX AAR21922
ID AAR21922 standard; Protein: 146 AA.
XX AC AAR21922;
XX DT 13-APR-1992 (first entry)
XX DE Leu(2) human beta-globin mutant.
XX KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
KW NA2 (2) His to Ieu.
XX OS Homo sapiens.
XX PN WO9119505-A.
XX PR 26-DEC-1991.
XX PF 20-JUN-1991; 91WO-US04156.
XX PR 20-JUN-1990; 90US-0541011.
XX PA (RESE) RES CORP TECHN INC.
XX PI Fronticelli C, Bucci E, Brinigar W;
XX DR WPI; 1992-024191/03.
XX PT Modified beta-chain of human haemoglobin - with aminoacid changes
PT to reduce oxygen affinity, used in blood prods. for transfusion,
PT with enhanced chloride sensitivity
XX PS Claim 19; Page 63; 87pp; English.
XX CC The modified beta-globin chain differs from the wild-type protein
CC sequence in that it has His at position 2 replaced by Leu. It is
one of the preferred mutant proteins covered by the invention having

CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.
 XX
 SQ Sequence 146 AA;

Qy	1	LVVYPWTQRF 10	Score 10; DB 13; Length 146; Best Local Similarity 100.0%; Pred. No. 0.00019; Indels 0; Gaps 0; Matches 10; Conservative 0; Mismatches 0;	Indels 0; Gaps 0;
Db	32	lvvypwtqrf 41		

RESULT 68

AAR1923	ID	AAR21923 standard; Protein; 146 AA.	XX
AC	XX		DE Asp(2) human beta-globin mutant.
DT	XX		XX
13-APR-1992	(first entry)		DE
PR	XX		XX
20-JUN-1990;	90US-0541011.		KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
PA	XX		NA2 (2) His to Asp.
Fronticelli C,	Bucci E,	Brinigar W;	XX OS Homo sapiens.
DR	XX		PN WO9119505-A.
PT	XX		PD 26-DEC-1991.
PT	XX		PF 20-JUN-1991; 91WO-US041156.
PT	XX		PR 20-JUN-1990;
PS	XX		DR 20-JUN-1990; 90US-0541011.
CC	XX		PA (RESE) RES CORP TECHN INC.
CC	XX		Fronticelli C, Bucci E, Brinigar W;
CC	XX		WPI; 1992-024191/03.
CC	XX		PT Modified beta-chain of human haemoglobin - with aminoacid changes to reduce oxygen affinity, used in blood prods. for transfusion, with enhanced chloride sensitivity
CC	XX		PT Claim 19; Page 63; 87pp; English.
CC	XX		CC The modified beta-chain of human haemoglobin - with aminoacid changes sequence in that it has His at position 2 replaced by Asp. It is one of the preferred mutant proteins covered by the invention having reduced oxygen affinity compared to wild-type beta-chain.
CC	XX		CC See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.
SQ	XX	Sequence 146 AA;	XX

(RESE) RES CORP TECHN INC.

Fronticelli C, Bucci E, Brinigar W;

WPI; 1992-024191/03.

Modified beta-chain of human haemoglobin - with aminoacid changes
sequence in that it has His at position 2 replaced by Asp. It is
one of the preferred mutant proteins covered by the invention having
reduced oxygen affinity compared to wild-type beta-chain.

See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.

Sequence 146 AA;

RESULT 70

AAR1925	ID	AAR21925 standard; Protein; 146 AA.	XX
AC	XX		AC AAR1925;
DT	XX		XX
13-APR-1992	(first entry)		DE
PR	XX		XX
20-JUN-1991;	91WO-US041156.		KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb.
PA	XX		XX OS Homo sapiens.
Fronticelli C,	Bucci E,	Brinigar W;	XX PN WO9119505-A.
DR	XX		PD 26-DEC-1991.
PT	XX		XX PF 20-JUN-1991; 91WO-US041156.
PT	XX		PR 20-JUN-1990;
PS	XX		PA (RESE) RES CORP TECHN INC.
Fronticelli C, Bucci E, Brinigar W;	XX		XX

Query Match 100.0%; Score 10; DB 13; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy	1	LVVYPWTQRF 10	Score 10; DB 13; Length 146; Best Local Similarity 100.0%; Pred. No. 0.00019; Indels 0; Gaps 0; Matches 10; Conservative 0; Mismatches 0;	Indels 0; Gaps 0;
Db	32	lvvypwtqrf 41		

RESULT 69

ARR1924	ID	ARR21924 standard; Protein; 146 AA.	XX
AC	XX		AC AAR21924;

	Best Local Similarity	Score	Pred.	No.	Mismatches	Indels	Gaps
DR	100.0%	10	0.00019	0	0	0	0;
ID	1	LWVYPWTQRF	10				
XX							
QY	1	LWVYPWTQRF	10				
DB	32	lvvypwtqrf	41				
RESULT	73						
AAR21927							
ID	AAR21927	standard; Protein	146 AA.				
XX							
AC	AAR21927;						
DT	13-APR-1992	(first entry)					
XX							
DE	Met(1), Tyr(2) human beta-globin mutant.						
XX	KW	autoxidation; beta-globin; blood transfusion; haemoglobin; Hb.					
XX	OS	Homo sapiens.					
XX	PN	W09119505-A.					
XX	PD	26-DEC-1991.					
XX	PF	20-JUN-1991; 91WO-US041156.					
XX	PR	20-JUN-1990; 90US-0541011.					
XX	PA	(RESE) RES CORP TECHN INC.					
XX	PI	Fronticelli C, Bucci E, Brinigar W;					
XX	DR	WPI; 1992-024191/03.					
XX	PT	Modified beta-chain of human haemoglobin - with aminoacid changes					
XX	PT	to reduce oxygen affinity, used in blood prods. for transfusion,					
XX	PT	with enhanced chloride sensitivity					
XX	PS	Claim 20; Page 63; 87pp; English.					
XX	CC	The modified beta-globin chain differs from the wild-type protein					
CC	CC	sequence in that it has Val at position 1 replaced by Met and His at					
CC	CC	position 2 replaced by Asp. It is one of the preferred mutant proteins					
CC	CC	covered by the invention having reduced oxygen affinity compared to					
CC	CC	wild-type beta-chain.					
CC	CC	See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.					
XX	SQ	Sequence 146 AA;					
PS	Claim 20; Page 63; 87pp; English.						
XX	Query Match	100.0%	Score	10	DB 13;	Length	146;
XX	Best Local Similarity	100.0%	Pred.	No.	0.00019;	Mismatches	
XX	Matches	10;	Conservative	0;			
XX	Indels	0;	Gaps	0;			
XX	Gaps	0;					
QY	1	LWVYPWTQRF	10				
DB	32	lvvypwtqrf	41				
RESULT	73						
AAR21928							
ID	AAR21928	standard; Protein	146 AA.				
XX							
AC	AAR21928;						
XX	DT	13-APR-1992 (first entry)					
XX	DE	Leu(1), Leu(2) human beta-globin mutant.					
XX	KW	autoxidation; beta-globin; blood transfusion; haemoglobin; Hb.					
XX							

Query Match 100.0%; Score 10; DB 13; Length 146;

Query Match 100.0%; Score 10; DB 13; Length 146;

OS Homo sapiens.
 XX
 PN WO9119505-A.
 XX
 PD 26-DEC-1991.
 XX
 PF 20-JUN-1991; 91WO-US04156.
 PR 20-JUN-1990; 90US-0541011.
 XX
 PA (RESE) RES CORP TECHN INC.
 XX
 PT Fronticelli C, Bucci E, Brinigar W;
 XX
 DR WPI; 1992-024191/03.

Modified beta-chain of human haemoglobin - with aminoacid changes to reduce oxygen affinity, used in blood prods. for transfusion, with enhanced chloride sensitivity

XX
 PS Claim 20; Page 63; 87pp; English.
 XX
 CC The modified beta-globin chain differs from the wild-type protein sequence in that it has Val at position 1 replaced by Leu and His at position 2 replaced by Asp. It is one of the preferred mutant proteins covered by the invention having reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAO20236-8, AAR20300-R20317 and AAR21914-R21930.
 XX
 PA Sequence 146 AA;

XX
 PT Fronticelli C, Bucci E, Brinigar W;
 XX
 DR WPI; 1992-024191/03.

Modified beta-chain of human haemoglobin - with aminoacid changes to reduce oxygen affinity, used in blood prods. for transfusion, with enhanced chloride sensitivity

XX
 PS Claim 20; Page 63; 87pp; English.
 XX
 CC The modified beta-globin chain differs from the wild-type protein sequence in that it has Val at position 1 replaced by Leu and His at position 2 replaced by Leu. It is one of the preferred mutant proteins covered by the invention having reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAO20236-8, AAR20300-R20317 and AAR21914-R21930.
 XX
 PA Sequence 146 AA;

XX
 Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ID 32 lvvypwtqrf 41

QY 1 LVVYPWTQRF 10
 DB 32 lvvypwtqrf 41

RESULT 74

Query Match	Score	DB	Length	Pred. No.	Mismatches	Indels	Gaps
Best Local Similarity	100.0%	13	146	0.00019	0	0	0
Matches	10						
Conservative	0						
Mismatches	0						
Indels	0						
Gaps	0						

CC Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ID 32 lvvypwtqrf 41

QY 1 LVVYPWTQRF 10
 DB 32 lvvypwtqrf 41

RESULT 75

Query Match	Score	DB	Length	Pred. No.	Mismatches	Indels	Gaps
Best Local Similarity	100.0%	13	146	0.00019	0	0	0
Matches	10						
Conservative	0						
Mismatches	0						
Indels	0						
Gaps	0						

CC Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ID 32 lvvypwtqrf 41

QY 1 LVVYPWTQRF 10
 DB 32 lvvypwtqrf 41

XX
 AC AAR21930;
 XX
 DT 13-APR-1992 (first entry)
 XX
 DE Leu(1), Tyr(2) human beta-globin mutant.
 XX
 KW autoxidation; beta-globin; blood transfusion; haemoglobin; hb.
 XX
 OS Homo sapiens.
 XX
 PN WO9119505-A.
 XX
 PD 26-DEC-1991.
 XX
 PF 20-JUN-1991; 91WO-US04156.
 XX
 PR 20-JUN-1990; 90US-0541011.
 XX
 PA (RESE) RES CORP TECHN INC.
 XX
 PI Fronticelli C, Bucci E, Brinigar W;
 XX
 DR WPI; 1992-024191/03.

Modified beta-chain of human haemoglobin - with aminoacid changes to reduce oxygen affinity, used in blood prods. for transfusion, with enhanced chloride sensitivity

XX
 PS Claim 20; Page 63; 87pp; English.
 XX
 CC The modified beta-globin chain differs from the wild-type protein sequence in that it has Val at position 1 replaced by Leu and His at position 2 replaced by Tyr. It is one of the preferred mutant Proteins covered by the invention having reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAO20236-8, AAR20300-R20317 and AAR21914-R21929.
 XX
 PA Sequence 146 AA;

XX
 Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ID 32 lvvypwtqrf 41

QY 1 LVVYPWTQRF 10
 DB 32 lvvypwtqrf 41

SQ sequence 146 AA;

Query Match 100.0%; Score 10; DB 14; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0;
Matches 10; Conservative 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
||||||||
Db 32 lvvypwtqrf 41

RESULT 83

ID AAR30532 standard; protein; 146 AA.

XX

AC AAR30532;

XX

DT 13-MAY-1993 (first entry)

DE Root effect beta globin.

XX

KW Globin; haemoglobin; Hb; affinity; oxygen; delivery; stroke; myocardial infarction; diabetes; tumour; X-ray treatment; burns; free radical; lesion.

XX

OS Homo sapiens.

FH Location/Qualifiers

FT Misc-difference 90

FT /label= E90V

FT Misc-difference 91

FT /label= L91M

FT Misc-difference 93

FT /label= C93S

FT Misc-difference 94

FT /label= D90E

FT US513426-A.

PN XX

PD 22-DEC-1992.

XX

PP 06-OCT-1989; 89US-0417949.

PR 06-OCT-1989; 89US-0417949.

PA (UYYA) UNIV YALE.

XX

PI Baserga SJ, Fischer JJ;

DR WPI; 1993-017570/02.

XX

PT New polynucleotide(s) coding for mutant globin chains - form haemoglobin with reduced oxygen affinity, useful e.g. for increasing oxygenation of tumour cells

PS Disclosure; Column 7; 11pp; English.

The sequences given in AAR30527-33 represent mutant globin molecules which when part of a haemoglobin (Hb) molecule, produces a mutant Hb with a lower affinity for oxygen than normal Hb. The oxygen affinity of the mutant Hb's being characterised by P50 of 30 torr to 3 atmos. and/or Hill coefficient of 2.5-1. The mutant Hb are useful for increasing oxygen delivery to tissue in patients suffering from myocardial infarction, stroke, diabetes etc. They may also be used to make tumours more susceptible to X-ray treatment by combining with free radicals and fixing the lesion in the cell. These Hb may be used to replace the Hb in an entire bloodstream and for treating burns patients.

SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 14; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0;
Matches 10; Conservative 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
||||||||
Db 32 lvvypwtqrf 41

RESULT 84

ID AAR32989 standard; protein; 146 AA.

XX

AC AAR32989;

XX

DT 17-JUN-1993 (first entry)

DE Human beta Haemoglobin and petunia EPSP synthase transit peptide.

XX

KW Recombinant products; commercial production; fermentation; biosynthesis; natural products; recombinant proteins; product expression; protein expression; expressed proteins.

OS Chimaeric - Homo sapiens.

XX

PN WO9303161-A.

XX

PD 18-FEB-1993.

XX

PP 31-JUL-1992; 92WO-US06359.

XX

PR 01-AUG-1991; 91US-0739143.

XX

PA (DASM;) DAWSON W O.
(DONSON;) DONSON J.
(GARGER;) GARGER S J.
(GRANTHAM;) GRANTHAM G L.
(GRILLE;) GRILLE L K.
(TURPEN;) TURPEN A M.
(TURPEN;) TURPEN T H.

XX

PI Dawson WO, Donson J, Garger SJ, Grantham GL, Grille LK;

PI Turpenam, Turpen TH;

XX

DR WPI; 1993-076518/09.

DR N-PSB; Q376810.

XX

PT Recombinant plant viral nucleic acids - used to express a prod..

PT e.g. antibody or IL-1 in a plant

XX

PS Example 4; Page 105; 30pp; English.

CC This sequence is human beta-haemoglobin with petunia EPSP synthase transit peptide. The coding sequence was inserted into recombinant plant viral nucleic acid which was then used to express a recombinant product (in this case human beta-Hb) in a plant. The plant viral sequence may be from tobacco mosaic, cucumber green mottle, cowpea mosaic, bromo mosaic, broad bean mottle, rice necrosis, geminiviruses, tomato golden mosaic, cassava latent and maize streak viruses.

SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 14; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0;
Matches 10; Conservative 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
||||||||
Db 32 lvvypwtqrf 41

XX
 PA
 (STRO-) STROTECH INC.
 PT
 XX
 PI
 Bajwa W., De Angelo J., Motwani NM;
 XX
 DR
 WPI: 1993-167394/70.
 XX
 New haemoglobin variants bind reversibly to oxygen - useful as
 PT physiological oxygen carriers (e.g. in blood substitutes) and as
 PT plasma expanders
 PS Disclosure; Page 13; 211PP; English.
 XX
 CC The sequences given in AAR39721-28 represent variant haemoglobins
 derived from embryonic zeta, embryonic epsilon, fetal gamma, adult
 delta, adult alpha and adult beta haemoglobins. The variants HbF
 Chico, Hb Portland Titusville and Hb BoVII have lower oxygen affinity,
 HbA Deer Lodge, HbA Abruzzo and HbA McKees Rock have higher oxygen
 affinity. HbA Motown/Haceteppe is an alkaline stable variant compared
 to the wild type molecules, and a further variant was produced which
 had a lower oxygen affinity and was stable in alkali. The DNA
 sequences encoding these globin variants may be used to transform
 yeast such that they produce the globins. The variant globins may
 be used in applications which require physiological oxygen carriers,
 such as in blood substitute solutions, or as plasma expanders.
 CC
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 14; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0 00019; Mismatches 10; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWQRF 10
 OY |||||||
 Db 32 Lvvypwqrf 41

RESULT 92
 AAR39458 ID AAR39458 standard; Protein: 146 AA.
 XX
 AC AAR39458;
 XX 09-SEP-1993 (first entry)
 DE Des-Val beta globin.
 XX
 KW PSE1.1E4; multimeric haemoglobin; pseudotetramer;
 KW crosslinking cysteine; blood.
 OS Synthetic.

FH Key Location/Qualifiers
 FT Misc-difference 2.4
 FT /note= "potential sites for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 6 /note= "potential site for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 12..13 /note= "potential sites for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 9 /note= "potential site for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 16..22 /note= "potential sites for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 43..44 /note= "potential sites for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 47 /note= "potential sites for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"

FT /note= "potential site for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 49..50 /note= "potential sites for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 52..53 /note= "potential sites for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 59 /note= "potential site for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 61..62 /note= "potential sites for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 65..66 /note= "potential sites for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 72..73 /note= "potential sites for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 76..80 /note= "potential sites for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 83 /note= "potential site for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 86..87 /note= "potential sites for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 90 /note= "potential sites for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 95 /note= "potential site for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 116..117 /note= "potential sites for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 120..121 /note= "potential site for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 123 /note= "potential site for Xaa -> Cys mutation
 to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 131..146 /note= "site where formation of two disulfide bonds
 (or per subunit) would be sterically hindered,
 so use of a di-alpha or di-beta construction
 is unnecessary"
 FT
 FT Misc-difference 11..40 /note= "candidate sites for mutation to block
 haptoglobin binding"
 FT
 FT Misc-difference 131..146 /note= "candidate sites for mutation to block
 haptoglobin binding"
 FT
 XX WO9309143-A.
 XX
 PD 13-MAY-1993.
 XX
 PR 06-NOV-1992;
 XX 92WO-US09152.
 XX
 PR 08-NOV-1991;
 XX 91US-0789179.
 PA (SOMA-) SOMATOGEN INC.
 XX
 PI Anderson DC, Mathews AJ, Stettler GL;
 XX
 DR WPI: 1993-167626/20.
 DR N-PSDB; AAQ42395.
 XX
 PT Non-natural multimeric haemoglobin-like protein - based on
 pseudo-tetramer contg. pseudo-dimer polypeptide with globin-like

PT domains, used to prolong haemoglobin half life and supplement
 PT oxygen carrying capacity of blood
 XX

PS Disclosure; Fig 2; 161pp; English.

XX

CC The pref. synthetic gene for expression of (des-Val)-alpha-(Gly)-
 CC alpha and des-Val beta globin is carried by pSGE1.14. The first
 CC alpha globin sequence begins with "Met-Leu", that is, it contains
 CC an artifactual methionine, omits the valine which is the normal
 CC first residue of mature alpha globin, and continues with the
 CC second residue, leucine. The second alpha globin sequence begins
 CC with "Val-Ieu", immediately after the linker.
 CC The Xaa -> Cys mutations should be made asymmetrically, i.e., only
 CC one region of a di-alpha or di-beta gene, so only one crosslink is
 CC added per tetramer.
 XX

SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 14; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; DE Human beta haemoglobin.
 QY 1 LVVYPWTQRF 10
 Db 32 lvvypwtqrf 41

RESULT 93
 AAR42632 standard; Protein: 146 AA.
 ID AAR42632;
 XX
 AC AAR42632;
 DT 26-APR-1994 (first entry)
 XX
 DE Natural beta-globin.
 XX
 KW Haemoglobin; alpha globin; beta globin; blood substitute;
 KW oxygen carrier; reversible oxygen fixation; chimeric gene;
 KW fusion protein.
 XX
 WO9319089-A.
 PN 30-SEP-1993.
 XX
 PR 1B-MAR-1993; 93W0-FR00273.
 XX
 PR 18-MAR-1992; 92FRR-0003224.
 XX
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (INMR) PASTEUR MERIEUX SERUMS & VACCINS.
 XX
 PI Edelstein S, Pagnier RJ, Poyart C;
 XX
 DR WPI; 1993-320682/40.
 DR N-PSDB; AAQ95616.

XX
 PT New synthetic tetrameric globin type oxygen transporter - with
 all chains identical and contg. haem, useful as blood substitute
 for transfusion
 PT Disclosure; Fig 2; 41pp; French.

XX
 CC Chimeric alpha-beta globin molecules are claimed which, when
 associated together to reconstitute the alpha1-beta2 interface and
 incorporating haem, are suitable as blood substitutes. Pref. the
 CC chimeric chains contain amino acids 1'-73 of beta globin at the
 CC N-terminus and amino acids 69 onwards of alpha-globin at the
 CC C-terminus. Alternatively, each chain may contain the N-terminus of
 CC an alpha chain with the C-terminus of a beta-chain, or all 4
 CC chains can be of the beta type. The tetramers are characterised by
 a lower oxygen affinity than natural haemoglobin.

XX
 Sequence 146 AA;

Query Match 100.0%; Score 10; DB 14; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; DE Human beta haemoglobin.
 QY 1 LVVYPWTQRF 10
 Db 32 lvvypwtqrf 41

RESULT 94
 AAR55132 standard; Protein: 146 AA.
 ID AAR55132;
 XX
 AC AAR55132;
 XX
 DT 12-JAN-1995 (first entry)
 XX
 DE Virus; recombinant; Plant virus; alpha trichosanthin; Phenotype;
 KW virus; recombinant; Plant virus; alpha haemoglobin; bromo mosaic virus; gemini virus;
 KW alpha amylase; alpha haemoglobin; rice necrosis virus tobamovirus; gene expression; chinese cucumber;
 KW beta haemoglobin.
 XX
 OS Homo sapiens.
 XX
 US5316931-A.
 XX
 PN 31-MAY-1994.
 XX
 PR 26-FEB-1988; 88US-0160766.
 PR 26-FEB-1988; 88US-0160771.
 PR 15-JUL-1988; 88US-0219279.
 PR 17-FEB-1989; 89US-0310881.
 PR 05-MAY-1989; 89US-0347637.
 PR 08-JUN-1989; 89US-0361138.
 PR 22-OCT-1990; 90US-0600244.
 PR 16-JAN-1991; 91US-0611617.
 PR 26-JUL-1991; 91US-0737899.
 PR 01-AUG-1991; 91US-0739143.
 XX
 PA (BIOS-) BIOSOURCE GENETICS CORP.
 XX
 PI Dawson WO, Donson J, Garger SJ, Granthan GL, Grill LK;
 PT Turpen AM, Turpen TH;
 XX
 DR WPI; 1994-1762269/21.
 DR N-PSDB; AAQ65576.

XX
 PT New recombinant plant viral nucleic acid - capable of systemic
 PT infection and stable expression of non-native nucleic acid in
 PT plant host
 XX
 PS Example 4; Columns 59-62; 44pp; English.

XX
 CC The beta haemoglobin coding sequence was fused to a sequence
 CC encoding the petunia ERS2 synthase transit peptide and inserted into
 CC a recombinant plant virus which can then be used to infect plants
 CC for the production of non-native products (in this case human
 CC beta-haemoglobin). Other genes which may be inserted into the
 CC virus are those which control a phenotypic trait, such as male
 CC sterility, or sequences encoding anti-sense RNA which can be useful
 CC to prevent the expression of undesired phenotypic traits. The
 CC recombinant virus is derived from a plus sense, single stranded
 CC virus selected from tobamovirus, bromo mosaic virus, rice necrosis
 CC virus or a gemini virus.

SO	Sequence	146 AA:
Qy	1 LIVVPPWTQRF 10 11111111	Best Local Similarity 100.0%; Pred. No. 0.00019; Length 146; Mismatches 0; Indels 0; Gaps 0;
Db	32 lvvypwtqrf 41	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT	95	
AAR4522	AAR4522 standard; Protein: 146 AA.	
ID		
XX		
NC	AAR4522;	
XX		
DT	23-JUN-1994 (first entry)	
XX		
DE	Adult human beta-globin C112I.	
XX		
KW	Adult; pig; beta; globin; gene; regulatory region; promoter;	
KW	transgenic pig; human; alpha; haemoglobin; Hb; erythrocyte;	
KW	transfusion; human/pig; hybrid Hb.	
XX		
KW	Adult; pig; beta; globin; gene; regulatory region; promoter;	
KW	transgenic pig; human; alpha; haemoglobin; Hb; erythrocyte;	
KW	transfusion; human/pig; hybrid Hb.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 112	/label= C112I
XX		
PN	W09325071-A.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 115	/label= A115V
XX		
XX		
PN	W09325071-A.	
XX		
PD	23-DEC-1993.	
XX		
PF	11-JUN-1993;	93WO-US05629.
XX		
PR	12-JUN-1992;	92US-0897648.
PR	08-DEC-1992;	92US-0987990.
PR	15-MAR-1993;	93US-003097.
PR	(DNXD-) DNX CORP.	
XX		
PI	Holtzman SH, Keller H, Kumar R, Logan JS, O' Donnell JK;	
PI	Parsons CT, Pilder SH, Pinkert CA, Sharma A, Swanson ME;	
PT	White SP;	
XX		
PA	WPI: 1994-007075/01.	
XX		
PT	Transgenic pigs which produce human haemoglobin - contg. DNA encoding	
PT	human alpha globin and huma beta globin linked to promoters	
PS	Claim 15; ; 117pp; English.	
XX		
CC	The sequences given in AAR4521-28 represent mutant versions of the adult human beta globin sequence. These sequences were not given in the specification but were generated using the known beta globin sequence.	
CC	These sequences were used in the production of constructs which were used to produce the transgenic pigs of the invention. These constructs contain the pig beta globin promoter sequence operably linked to the human alpha or beta globin genes. Pigs containing these constructs express human haemoglobin (Hb) in their erythrocytes and are healthy, suffering no deleterious side effects as a result of heterologous Hb production. They can be used as an efficient and economical source of human Hb that can be used for transfusion and other medical applications. Also, a human/pig hybrid Hb can be produced which exhibits a P50 that is higher than that of native human or pig Hb.	
XX		
SO	Sequence 146 AA:	
Qy	1 LIVVPPWTQRF 10 11111111	Best Local Similarity 100.0%; Pred. No. 0.00019; Length 146; Mismatches 0; Indels 0; Gaps 0;
Db	32 lvvypwtqrf 41	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 32 ||||||| 1vvypwtqrf 41

RESULT 98
AAR4525

RESULT 97
AAR4524

ID AAR4524 standard; Protein: 146 AA.

ID AAR4525 standard; Protein: 146 AA.

ID AAR4525;

RESULT 98
AAR4525
ID AAR4525 standard; Protein: 146 AA.
XX
AC AAR4525;
XX
DT 23-JUN-1994 (first entry)
DE Adult human beta-globin A115L.
XX
KW Adult; pig; beta; globin; gene; regulatory region; promoter;
transgenic pig; human; alpha; haemoglobin; Hb; erythrocyte;
transfusion; human/pig; hybrid Hb.
XX
OS Homo sapiens.
XX
FH
FT Misc-difference 119
PH Location/Qualifiers
FT /label= A115L
FT
PN WO9325071-A.
XX
PD 23-DEC-1993.
XX
PF 11-JUN-1993;
XX
PR 12-JUN-1992;
PR 08-DEC-1992;
PR 15-MAR-1993;
PR 08-DEC-1992;
PR 15-MAR-1993;
PR (DNXD-) DNX CORP.
PA
XX
PR 12-JUN-1992;
PR 92US-0897648.
PR 08-DEC-1992;
PR 92US-0987890.
PR 15-MAR-1993;
PR 93US-0030897.
PA (DNXD-) DNX CORP.
XX
PI Holtzman SH, Keller H, Kumar R, Logan JS, O' Donnell JK;
PI Parsons CT, Pilder SH, Pinkert CA, Sharma A, Swanson ME;
PI White SP;
XX
DR WPI; 1994-007075/01.
XX
PT transgenic pigs which produce human haemoglobin - contg. DNA encoding
PT human alpha globin and huma beta globin linked to promoters
PS
XX
CC The sequences given in AAR4521-28 represent mutant versions of the
CC adult human beta globin sequence. These sequences were not given in the
CC specification but were generated using the known beta globin sequence.
CC These sequences were used in the production of constructs which were
CC used to produce the transgenic pigs of the invention. These constructs
CC contain the pig beta globin promoter sequence operably linked to the
CC human alpha or beta globin genes. Pigs containing these constructs
CC express human haemoglobin (Hb) in their erythrocytes and are healthy,
CC suffering no deleterious side effects as a result of heterologous Hb
CC production. They can be used as an efficient and economical source of
CC human Hb that can be used for transfusion and other medical
CC applications. Also, a human/pig hybrid Hb can be produced which
CC exhibits a P50 that is higher than that of native human or pig Hb.
XX
SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 10; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 10; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 10; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 10; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 10; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 10; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 32 1vvypwtqrf 41

RESULT 99
AAR4526
ID AAR4526 standard; Protein: 146 AA.
XX
AC AAR4526;
XX
DT 23-JUN-1994 (first entry)
DE Adult human beta-globin G119H.
XX
KW Adult; pig; beta; globin; gene; regulatory region; promoter;
transgenic pig; human; alpha; haemoglobin; Hb; erythrocyte;
transfusion; human/pig; hybrid Hb.
XX
OS Homo sapiens.
XX
FH
FT Misc-difference 119
PH Location/Qualifiers
FT /label= G119H
FT
PN WO9325071-A.
XX
PD 23-DEC-1993.
XX
PF 11-JUN-1993;
XX
PR 93WO-US05629.
XX
PR 12-JUN-1992;
PR 92US-0897648.
PR 08-DEC-1992;
PR 92US-0987890.
PR 15-MAR-1993;
PR 93US-0030897.
PA (DNXD-) DNX CORP.
XX
PI Holtzman SH, Keller H, Kumar R, Logan JS, O' Donnell JK;
PI Parsons CT, Pilder SH, Pinkert CA, Sharma A, Swanson ME;
PI White SP;
XX
DR WPI; 1994-007075/01.
XX
PT transgenic pigs which produce human haemoglobin - contg. DNA encoding
PT human alpha globin and huma beta globin linked to promoters
PS
XX
CC The sequences given in AAR4521-28 represent mutant versions of the
CC adult human beta globin sequence. These sequences were not given in the
CC specification but were generated using the known beta globin sequence.
CC These sequences were used in the production of constructs which were
CC used to produce the transgenic pigs of the invention. These constructs
CC contain the pig beta globin promoter sequence operably linked to the
CC human alpha or beta globin genes. Pigs containing these constructs
CC express human haemoglobin (Hb) in their erythrocytes and are healthy,
CC suffering no deleterious side effects as a result of heterologous Hb
CC production. They can be used as an efficient and economical source of
CC human Hb that can be used for transfusion and other medical
CC applications. Also, a human/pig hybrid Hb can be produced which
CC exhibits a P50 that is higher than that of native human or pig Hb.
XX
SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 10; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 10; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 10; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 10; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 10; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 32 1vvypwtqrf 41

RESULT 99
AAR4526
ID AAR4526 standard; Protein: 146 AA.

AC AAR44526;
 XX DE Adult human beta-globin Q131E.
 DT 23-JUN-1994 (first entry)
 XX KW Adult; pig; beta; globin; gene; regulatory region; promoter;
 DE KW transgenic pig; human; alpha; haemoglobin; Hb; erythrocyte;
 XX KW transfusion; human/pig; hybrid Hb.
 XX OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 128
 PT /label= P128M(sic)
 XX
 PN WO9325071-A.
 PD 23-DEC-1993.
 XX PF 11-JUN-1993; 93WO-US05629.
 XX PR 12-JUN-1992; 92US-0897648.
 PR 08-DEC-1992; 92US-0987890.
 PR 15-MAR-1993; 93US-0030897.
 XX PA (DNX1D-) DNX CORP.
 PR Holtzman SH, Keller H, Kumar R, Logan JS, O' Donnell JK;
 PI Parsons CT, Pilder SH, Pinkert CA, Sharma A, Swanson ME;
 PI White SP;
 PA (DNX1D-) DNX CORP.
 XX PI Holtzman SH, Keller H, Kumar R, Logan JS, O' Donnell JK;
 PT Parsons CT, Pilder SH, Pinkert CA, Sharma A, Swanson ME;
 PT White SP;
 DR WPI; 1994-007075/01.
 XX
 PT Transgenic pigs which produce human haemoglobin - contg. DNA encoding
 PT human alpha globin and huma beta globin linked to promoters
 XX
 PS Claim 15; 117pp; English.
 XX
 CC The sequences given in AAR44521-28 represent mutant versions of the
 adult human beta globin sequence. These sequences were not given in the
 specification but were generated using the known beta globin sequence.
 CC These sequences were used in the production of constructs which were
 used to produce the transgenic pigs of the invention. These constructs
 contain the pig beta globin promoter sequence operably linked to the
 human alpha or beta globin genes. Pigs containing these constructs
 express human haemoglobin (Hb) in their erythrocytes and are healthy,
 suffering no deleterious side effects as a result of heterologous Hb
 production. They can be used for transfusion and other medical
 applications. Also, a human/pig hybrid Hb can be produced which
 exhibits a p50 that is higher than that of native human or pig Hb.
 CC Sequence 146 AA;
 XX
 SQ Query Match 100.0%; Score 10; DB 15; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LVVVPWTQRF 10
 |||||||
 Db 32 lvvvpwtqrf 41
 |||||||
 XX
 RESULT 100
 AAR4527
 ID AAR4527 standard; Protein; 146 AA.
 XX
 AC AAR4527;
 XX
 DT 23-JUN-1994 (first entry)
 XX

Tue Jul 2 09:03:45 2002

us-09-147-490-1.rag

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 12:06:27 ; Search time 13:04 Seconds

(without alignments)
18.731 Million cell updates/sec

Title: US-09-147-490-1
Perfect score: 10
Sequence: 1 LVVVPPWPTQRF 10
Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 231628 seqs, 24425594 residues
Word size : 0
Total number of hits satisfying chosen parameters: 231628
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Issued_Patents_AA:
1: /cn2_6/podata/2/1aa/5A_COMB.pep: *
2: /cn2_6/podata/2/1aa/5B_COMB.pep: *
3: /cpn2_6/podata/2/1aa/6A_COMB.pep: *
4: /cn2_6/podata/2/1aa/6B_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	10	100.0	10	2 US-08-627-173-4
2	10	100.0	10	2 US-08-627-173-25
3	10	100.0	10	2 US-08-535-882A-4
4	10	100.0	10	2 US-09-535-882A-26
5	10	100.0	10	3 US-09-005-546-4
6	10	100.0	10	3 US-09-005-546-26
7	10	100.0	55	4 US-09-352-078-9
8	10	100.0	55	4 US-09-352-078-9
9	10	100.0	74	2 US-08-105-989-25
10	10	100.0	74	4 US-09-138-922-21
11	10	100.0	74	4 US-09-138-922-25
12	10	100.0	143	4 US-09-230-603-22
13	10	100.0	144	4 US-09-230-603-21
14	10	100.0	146	1 US-07-923-692C-0
15	10	100.0	146	1 US-08-170-095B-2
16	10	100.0	146	1 US-08-184-237-10
17	10	100.0	146	1 US-08-240-712-28
18	10	100.0	146	1 US-08-240-712-20
19	10	100.0	146	1 US-08-240-712-21
20	10	100.0	146	1 US-08-240-712-22
21	10	100.0	146	1 US-08-240-712-23
22	10	100.0	146	1 US-08-240-712-24
23	10	100.0	146	1 US-08-240-712-28
24	10	100.0	146	1 US-08-395-866-2
25	10	100.0	146	1 US-08-443-890-19
26	10	100.0	146	1 US-08-443-890-20
27	10	100.0	146	1 US-08-443-890-21

28	10	100.0	146	1 US-08-443-890-22	Sequence 22, Appli
29	10	100.0	146	1 US-08-443-890-23	Sequence 23, Appli
30	10	100.0	146	1 US-08-443-890-24	Sequence 24, Appli
31	10	100.0	146	1 US-08-443-890-28	Sequence 28, Appli
32	10	100.0	146	2 US-08-484-686B-66	Sequence 66, Appli
33	10	100.0	146	2 US-08-484-686B-67	Sequence 67, Appli
34	10	100.0	146	2 US-08-484-686B-68	Sequence 68, Appli
35	10	100.0	146	2 US-08-484-686B-70	Sequence 70, Appli
36	10	100.0	146	2 US-08-484-686B-70	Sequence 70, Appli
37	10	100.0	146	2 US-08-627-173-18	Sequence 18, Appli
38	10	100.0	146	2 US-08-627-173-22	Sequence 22, Appli
39	10	100.0	146	2 US-08-482-920-10	Sequence 10, Appli
40	10	100.0	146	2 US-08-535-882A-18	Sequence 18, Appli
41	10	100.0	146	2 US-08-535-882A-22	Sequence 22, Appli
42	10	100.0	146	2 US-08-619-708A-6	Sequence 4, Appli
43	10	100.0	146	3 US-08-316-424A-4	Sequence 8, Appli
44	10	100.0	146	3 US-08-316-424A-8	Sequence 2, Appli
45	10	100.0	146	3 US-08-381-175A-2	Sequence 8, Appli
46	10	100.0	146	3 US-08-381-175A-8	Sequence 8, Appli
47	10	100.0	146	3 US-08-484-341-10	Sequence 10, Appli
48	10	100.0	146	3 US-09-005-546-18	Sequence 18, Appli
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50	10	100.0	146	4 US-08-230-603-2	Sequence 2, Appli
51	10	100.0	146	4 US-08-230-603-12	Sequence 12, Appli
52	10	100.0	146	4 US-09-230-603-13	Sequence 13, Appli
53	10	100.0	146	4 US-09-230-603-17	Sequence 17, Appli
54	10	100.0	146	4 US-09-230-603-20	Sequence 20, Appli
55	10	100.0	146	4 US-08-463-160B-67	Sequence 67, Appli
56	10	100.0	146	4 US-08-463-160B-68	Sequence 68, Appli
57	10	100.0	146	4 US-09-230-603-12	Sequence 12, Appli
58	10	100.0	146	4 US-08-463-160B-71	Sequence 71, Appli
59	10	100.0	146	4 US-09-058-562-19	Sequence 19, Appli
60	10	100.0	146	4 US-09-058-562-20	Sequence 20, Appli
61	10	100.0	146	4 US-09-058-562-22	Sequence 22, Appli
62	10	100.0	146	4 US-09-058-562-26	Sequence 26, Appli
63	10	100.0	146	4 US-09-031-361-2	Sequence 2, Appli
64	10	100.0	146	4 US-08-483-502-10	Sequence 10, Appli
65	10	100.0	146	4 US-09-352-078-1	Sequence 1, Appli
66	10	100.0	146	4 US-08-983-564A-33	Sequence 3, Appli
67	10	100.0	146	5 PCT-US92-09752-19	Sequence 19, Appli
68	10	100.0	146	5 PCT-US92-09752-20	Sequence 20, Appli
69	10	100.0	146	5 PCT-US92-09752-21	Sequence 21, Appli
70	10	100.0	146	5 PCT-US92-09752-22	Sequence 22, Appli
71	10	100.0	146	5 PCT-US92-09752-23	Sequence 23, Appli
72	10	100.0	146	5 PCT-US92-09752-24	Sequence 24, Appli
73	10	100.0	146	5 PCT-US92-09752-28	Sequence 28, Appli
74	10	100.0	147	1 US-08-550-715-11	Sequence 11, Appli
75	10	100.0	147	4 US-09-230-603-14	Sequence 14, Appli
76	10	100.0	147	4 US-09-230-603-15	Sequence 15, Appli
77	10	100.0	147	4 US-09-230-603-16	Sequence 16, Appli
78	10	100.0	147	4 US-09-230-603-18	Sequence 18, Appli
79	10	100.0	147	4 US-09-230-603-19	Sequence 19, Appli
80	10	100.0	147	4 US-09-058-562-21	Sequence 21, Appli
81	10	100.0	147	4 US-08-627-173-5	Sequence 5, Appli
82	10	100.0	147	4 US-08-535-882A-5	Sequence 5, Appli
83	10	100.0	147	3 US-09-005-546-5	Sequence 5, Appli
84	9	90.0	146	2 US-08-627-173-20	Sequence 20, Appli
85	9	90.0	146	2 US-08-535-882A-20	Sequence 20, Appli
86	9	90.0	146	3 US-08-316-424A-6	Sequence 6, Appli
87	9	90.0	146	3 US-09-005-546-20	Sequence 20, Appli
88	8	80.0	146	2 US-08-627-173-6	Sequence 6, Appli
89	8	80.0	146	2 US-08-627-173-7	Sequence 7, Appli
90	8	80.0	146	2 US-08-535-882A-6	Sequence 7, Appli
91	8	80.0	146	2 US-08-535-882A-27	Sequence 7, Appli
92	8	80.0	146	3 US-09-005-546-6	Sequence 6, Appli
93	8	80.0	146	3 US-09-005-546-27	Sequence 7, Appli
94	7	70.0	146	2 US-08-627-173-7	Sequence 7, Appli
95	7	70.0	146	2 US-08-627-173-10	Sequence 11, Appli
96	7	70.0	146	2 US-08-627-173-11	Sequence 11, Appli
97	7	70.0	146	2 US-08-535-882A-7	Sequence 7, Appli
98	7	70.0	146	2 US-08-535-882A-10	Sequence 11, Appli
99	7	70.0	146	2 US-08-535-882A-11	Sequence 11, Appli
100	7	70.0	146	2 US-08-981-384-1	Sequence 11, Appli

ALIGNMENTS

ALIGNMENTS

RESULT 1
US-08-627-173-4
Sequence 4, Application US/08627173
PATENT NO. 5861483
GENERAL INFORMATION:
APPLICANT: TSIRLOVA, IRENA
APPLICANT: WOLPE, STEPHEN D.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,173
FILING DATE: 03-APR-1996
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,173
FILING DATE: 03-APR-1996
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

RESULT 2
US-08-627-173-4
Query Match 100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e-05; Mismatches 0;
Matches 10; Conservative 0; Indels 0; Gaps 0;
Type: amino acid
Strandedness:
Topology: linear
Molecule Type: peptide

Query Match 100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e-05; Mismatches 0;
Matches 10; Conservative 0; Indels 0; Gaps 0;
Type: amino acid
Strandedness:
Topology: linear
Molecule Type: peptide

RESULT 3
US-08-535-882A-4
Query Match 100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e-05; Mismatches 0;
Matches 10; Conservative 0; Indels 0; Gaps 0;
Type: amino acid
Strandedness:
Topology: linear
Molecule Type: peptide

Query Match 100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e-05; Mismatches 0;
Matches 10; Conservative 0; Indels 0; Gaps 0;
Type: amino acid
Strandedness:
Topology: linear
Molecule Type: peptide

RESULT 4
US-08-535-882A
Sequence 4, Application US/08535882A
Patent No. 5861483
GENERAL INFORMATION:
APPLICANT: TSIRLOVA, IRENA
APPLICANT: WOLPE, STEPHEN D.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,882A
FILING DATE: 28-SEP-1995
Classification: 435

ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-535-882A-4

Query Match 100.0%; Score 10; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2e-05; Mismatches 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVVPWTORF 10
 Db 1 LVVVPWTORF 10

RESULT 4

US-08-535-882A-26 Application US/08535882A

PATENT NO. 5939391
 GENERAL INFORMATION:
 APPLICANT: TSYRLOVA, IRENA
 APPLICANT: WOLPE, STEPHEN D.

TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 TITLE OF INVENTION: USES THEREOF
 NUMBER OF SEQUENCES: 27
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

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COUNTRY: U.S.A.

ZIP: 22201-4714

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/535,882
 FILING DATE: 28-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1331-177
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

RESULT 7
 US-09-352-078-9
 Query Match 100.0%; Score 10; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 |||||||
 Db 1 LVVYPWTQRF 10

GENERAL INFORMATION:
 APPLICANT: Theragen, Inc.
 APPLICANT: Hoffinan, Brian F.
 APPLICANT: Dubnick, Bernard
 TITLE OF INVENTION: USE OF MAMMALIAN-DERIVED PEPTIDES FOR
 TITLE OF INVENTION: THE TREATMENT OF MICROBIAL INFECTIONS
 FILE REFERENCE: 19441D0999US1
 CURRENT APPLICATION NUMBER: US/09/352,078
 CURRENT FILING DATE: 1999-07-14
 EARLIER APPLICATION NUMBER: PCT/US98/16746
 EARLIER FILING DATE: 1998-08-10
 EARLIER APPLICATION NUMBER: 60/061,454
 EARLIER FILING DATE: 1997-10-08
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 9
 LENGTH: 55
 TYPE: PRT
 ORGANISM: Homo sapiens

RESULT 7
 US-09-352-078-9
 Query Match 100.0%; Score 10; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 |||||||
 Db 1 LVVYPWTQRF 10

GENERAL INFORMATION:
 APPLICANT: Kumar, Ramesh
 APPLICANT: Sharma, Ajay
 APPLICANT: Paulhac, Clara
 APPLICANT: Khoury-Christianson, Anastasia P.
 APPLICANT: Midha, Sunita
 TITLE OF INVENTION: Production of Human Hemoglobin in
 TITLE OF INVENTION: Transgenic Pigs.
 NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
 ADDRESSEE: PENNIE & EDMONDS
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.

PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/535,882
 FILING DATE: 28-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1331-177
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

RESULT 7
 US-09-352-078-9
 Query Match 100.0%; Score 10; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 |||||||
 Db 1 LVVYPWTQRF 10

GENERAL INFORMATION:
 APPLICANT: Theragen, Inc.
 APPLICANT: Hoffinan, Brian F.
 APPLICANT: Dubnick, Bernard
 TITLE OF INVENTION: USE OF MAMMALIAN-DERIVED PEPTIDES FOR
 TITLE OF INVENTION: THE TREATMENT OF MICROBIAL INFECTIONS
 FILE REFERENCE: 19441D0999US1
 CURRENT APPLICATION NUMBER: US/09/352,078
 CURRENT FILING DATE: 1999-07-14
 EARLIER APPLICATION NUMBER: PCT/US98/16746
 EARLIER FILING DATE: 1998-08-10
 EARLIER APPLICATION NUMBER: 60/061,454
 EARLIER FILING DATE: 1997-10-08
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 9
 LENGTH: 55
 TYPE: PRT
 ORGANISM: Homo sapiens

RESULT 7
 US-09-352-078-9
 Query Match 100.0%; Score 10; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 |||||||
 Db 1 LVVYPWTQRF 10

GENERAL INFORMATION:
 APPLICANT: Kumar, Ramesh
 APPLICANT: Sharma, Ajay
 APPLICANT: Paulhac, Clara
 APPLICANT: Khoury-Christianson, Anastasia P.
 APPLICANT: Midha, Sunita
 TITLE OF INVENTION: Production of Human Hemoglobin in
 TITLE OF INVENTION: Transgenic Pigs.
 NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
 ADDRESSEE: PENNIE & EDMONDS
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.

RESULT 8

ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/105,989
 FILING DATE: 11-AUG-1993
 CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 6794-030
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 21:

INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 74 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 6794-030
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864/9741
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 74 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match 100.0%; Score 10; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 0.0001; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY	1	LVVPWPWTFR	10
	1		
Db	2	LVVPWPWTFR	11

RESULT 10
 US-09-138-922-21
 Sequence 25, Application US/09138922
 Patent No. 6147202

GENERAL INFORMATION:
 APPLICANT: Kumar, Ramesh
 APPLICANT: Sharma, Ajay
 APPLICANT: Khouri-Christiansen, Anastasia P.
 APPLICANT: Midha, Sunita

TITLE OF INVENTION: Production of Human Hemoglobin in Transgenic Pigs.
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PENNIE & EDMONDS
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/138,922
 FILING DATE: 11-AUG-1993
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/105,989
 FILING DATE: 11-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 6794-030
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 74 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 6794-030
 TELECOMMUNICATION INFORMATION:
 APPLICATION NUMBER: US/08/105,989
 FILING DATE: 11-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 6794-030

Query Match 100.0%; Score 10; DB 4; Length 74;
 Best Local Similarity 100.0%; Pred. No. 0.0001; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Db	Qy
1	LVWVPMWTQRF 10
2	LWVWPMWTQRF 11

OTHER INFORMATION: during the translation initiation step is excised
OTHER INFORMATION: during the translation initiation and is not present in the
OTHER INFORMATION: mature polypeptide chain

RESULT 12
US-09-230-603-22
Sequence 22, Application US/09230603
; Patent No. 6171826
; GENERAL INFORMATION:
; APPLICANT: LEVINE, JOSEPH D
; APPLICANT: APOSTOL, IZIDOR A

```

Query Match          100.0%; Score 10; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy   1 LVVYPWMTQRF 10
     ||||||||| 1
Db   33 LVVYPWMTQRF 42

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FILE REFERENCE: BXBFB3060
 CURRENT APPLICATION NUMBER: US/09/230,603
 CURRENT FILING DATE: 1999-05-14
 EARLIER APPLICATION NUMBER: PCT/US97/13564
 EARLIER FILING DATE: 1997-08-01
 EARLIER APPLICATION NUMBER: 60/023,211
 EARLIER FILING DATE: 1996-08-02
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 22
 LENGTH: 143
 TYPE: PRT
 ORGANISM: Escherichia coli
 FEATURE:
 NAME/KEY: NON_TER
 LOCATION: (1)
 OTHER INFORMATION: the N-terminal methionine residue incorporated
 OTHER INFORMATION: during the translation initiation step is excised
 OTHER INFORMATION: during translation and is not present in the
 OTHER INFORMATION: mature polypeptide chain
 US-09-230 603-22

RESULT 13
 US-09-230-603-21
 sequence 21; Application US/09230603
 Patent No. 6,171,826
 GENERAL INFORMATION:
 APPLICANT: LEVINE, JOSEPH D
 APPLICANT: APOSTOL, IZIDOR A
 TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
 TITLE OF INVENTION: HEMOGLOBIN
 FILE REFERENCE: BXFB3060
 CURRENT APPLICATION NUMBER: US/09/230,603
 CURRENT FILING DATE: 1999-05-14
 EARLIER APPLICATION NUMBER: PCT/US97/13564
 EARLIER FILING DATE: 1997-08-01
 EARLIER APPLICATION NUMBER: 60/023,211
 EARLIER FILING DATE: 1996-08-02
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 21
 LENGTH: 144
 TYPE: PRT
 ORGANISM: Escherichia coli
 FEATURE:
 NAME/KEY: NON_TER
 LOCATION: (1)
 OTHER INFORMATION: the N-terminal methionine residue incorporated

RESULT 14
US-07-923-692C-10
; Sequence 10, Application US/07923692C
; Patent No. 5316931
GENERAL INFORMATION:
APPLICANT: Dawson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Gager, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923, 692C
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600, 244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641, 617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310, 881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160, 766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160, 771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347, 637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363, 138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219, 279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Hallum, Albert P.
REGISTRATION NUMBER: 28, 957
REFERENCE/DOCKET NUMBER: BIOG-20121

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-433-4150

TELEFAX: 415-433-8716

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 146 amino acids

TYPE: amino acid

TOPOLGY: linear

MOLECULE TYPE: protein

US-07-923-692C-10

Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10

Db 32 LVVYPWTQRF 41

RESULT 15 US-08-170-095B-2

; Sequence 2, Application US/08170095B

Patient No. 5563254

GENERAL INFORMATION:

APPLICANT: Hoffman, Stephen J.

APPLICANT: Nagei, Kiyoshi

TITLE OF INVENTION: Blood Substitutes

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Somatogen, Inc.

STREET: 2545 Central Avenue

CITY: Boulder

STATE: Colorado

ZIP: 80301

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage

COMPUTER: Apple Macintosh

OPERATING SYSTEM: System 7.0.1

SOFTWARE: Microsoft Word 5.0a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/170,095B

FILING DATE: December 20, 1993

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: No. 5563254ak, Henry P.

REGISTRATION NUMBER: 33200

REFERENCE/DOCKET NUMBER: Hoffman 2A/CONT2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 303-444-3013

TELEFAX: 303-541-3322

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 146

TYPE: amino acid

STRANDEDNESS: single

TOPOLGY: unknown to applicant

MOLECULE TYPE: protein

HYPOTHETICAL: no

US-08-170-095B-2

Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10

Db 32 LVVYPWTQRF 41

US-08-184-237-10
; Sequence 10; Application US/08184237
; Patent No. 589367
GENERAL INFORMATION:
APPLICANT: Dawson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Gauger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,237
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 923,692
FILING DATE: 31-JUL-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BLOG-20121 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 41415-433-4150
TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLGY: linear
MOLECULE TYPE: protein
US-08-184-237-10

Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10

Db 32 LVVYPWTQRF 41

RESULT 16

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 17
US-08-240-712-19
; Sequence 19, Application US/08240712
; Patent No. 5599907
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DAVID C.
; APPLICANT: MATHEWS, ANTONY JAMES
; APPLICANT: STETLER, GARY L.
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
; TITLE OF INVENTION: HEMOGLOBINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brody and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patientin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,712
; FILING DATE: 09-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09752
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: ANDERSON=6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPology: linear
; MOLECULE TYPE: peptide
; US-08-240-712-19

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 18
US-08-240-712-20
; Sequence 20, Application US/08240712
; Patent No. 5599907
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DAVID C.
; APPLICANT: MATHEWS, ANTONY JAMES
; APPLICANT: STETLER, GARY L.
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
; TITLE OF INVENTION: HEMOGLOBINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brody and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patientin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,712

FILING DATE: 09-MAY-1994
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/09752
 FILING DATE: 13-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: COOPER, IVER P
 REGISTRATION NUMBER: 28, 005
 REFERENCE/DOCKET NUMBER: ANDERSON=6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-240-712-21

RESULT 20
 US-08-240-712-22
 ; Sequence 22, Application US/08240712
 ; Patent No. 5599907
 GENERAL INFORMATION:
 APPLICANT: ANDERSON, DAVID C.
 APPLICANT: MATHEWS, ANTONY JAMES
 APPLICANT: STEELER, GARY L.
 TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Browdy and Neimark
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/240,712
 FILING DATE: 09-MAY-1994
 CLASIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/09752
 FILING DATE: 13-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: COOPER, IVER P
 REGISTRATION NUMBER: 28, 005
 REFERENCE/DOCKET NUMBER: ANDERSON=6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-240-712-23

RESULT 21
 US-08-240-712-23
 ; Sequence 23, Application US/08240712
 ; Patent No. 5599907
 GENERAL INFORMATION:
 APPLICANT: ANDERSON, DAVID C.
 APPLICANT: MATHEWS, ANTONY JAMES
 APPLICANT: STEELER, GARY L.
 TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Browdy and Neimark
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/240,712
 FILING DATE: 09-MAY-1994
 CLASIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/09752
 FILING DATE: 13-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: COOPER, IVER P
 REGISTRATION NUMBER: 28, 005
 REFERENCE/DOCKET NUMBER: ANDERSON=6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-240-712-23

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVPPWQRF 10
 Db 32 LVVPPWQRF 41

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVPPWQRF 10
 Db 32 LVVPPWQRF 41

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVPPWQRF 10
 Db 32 LVVPPWQRF 41

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVPPWQRF 10
 Db 32 LVVPPWQRF 41

RESULT 22
US-08-240-712-24
SEQUENCE 24, Application US/08240712
PATENT NO. 5599907
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHERS, ANTHONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brody and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240.712
FILING DATE: 09-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEX: 248633
TELEFAX: 202-37-3728
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-240-712-24

RESULT 23
US-08-240-712-28
Sequence 28, Application US/08240712
Patent No. 5599907
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHERS, ANTHONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.

Query Match **Score 10;** **DB 1;** **Length**
Best Local Similarity 100.0%; Pred. No. 0.0018; **DB 1;** **Length**
Matches 10; Conservative 0; Mismatches 0; Inde-
Oy 1 LVVYPWTFQR 10

Db 32 LVVYPWTFQR 41

COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08/240,712
FILING DATE: 09-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON=6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-240-712-28

TELECOMMUNICATION INFORMATION:

TELEPHONE: 303-541-3322

TELEFAX: 303-444-3013

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 146

TYPE: amino acid

TOPOLOGY: unknown to applicant

MOLECULE TYPE: protein

HYPOTHETICAL: no

US-08-396-866-2

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0;
 Matches 10; Conservative 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTORF 10
Db 32 LVVYPWTORF 41RESULT 25
US-08-443-890-19Sequence 19, Application US/08443890
PATENT NO. 5739011

GENERAL INFORMATION:

APPLICANT: ANDERSON, DAVID C.

APPLICANT: MATHERS, ANTONY JAMES

APPLICANT: STETLER, GARY L.

TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC

TITLE OF INVENTION: HEMOGLOBINS

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brody and Neimark

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/443,890

FILING DATE: 31-MAY-1995

CLASSIFICATION: 530

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/240,712

FILING DATE: 09-MAY-1994

APPLICATION NUMBER: -PCT/US92/09752

FILING DATE: 13-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, IVER P

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: ANDERSON=6

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 146 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-08-443-890-20

Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTORF 10
Db 32 LVVYPWTORF 41RESULT 26
US-08-443-890-20Sequence 20, Application US/08443890
PATENT NO. 5739011

GENERAL INFORMATION:

APPLICANT: ANDERSON, DAVID C.

APPLICANT: MATHERS, ANTONY JAMES

APPLICANT: STETLER, GARY L.

TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC

TITLE OF INVENTION: HEMOGLOBINS

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brody and Neimark

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/443,890

FILING DATE: 31-MAY-1995

CLASSIFICATION: 530

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/240,712

FILING DATE: 09-MAY-1994

APPLICATION NUMBER: -PCT/US92/09752

FILING DATE: 13-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, IVER P

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: ANDERSON=6

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 146 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-08-443-890-21

Sequence 21, Application US/08443890

PATENT NO. 5739011

GENERAL INFORMATION:

APPLICANT: ANDERSON, DAVID C.

Query Match

100.0%; Score 10; DB 1; Length 146;

; Sequence 19, Application US/08443890

; Patent No. 5739011

; GENERAL INFORMATION:

; APPLICANT: ANDERSON, DAVID C.

; REGISTRATION NUMBER: 28,005

; REFERENCE/DOCKET NUMBER: ANDERSON=6

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

APPLICANT: MATHEWS, ANTONY JAMES
 APPLICANT: STETLER, GARY L.
 TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC HEMOGLOBINS
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Browdy and Neimark
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/443,890
 FILING DATE: 31-MAY-1995
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/240,712
 FILING DATE: 09-MAY-1994
 APPLICATION NUMBER: PCT/US92/09752
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/443,890
 FILING DATE: 31-MAY-1995
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/240,712
 FILING DATE: 09-MAY-1994
 APPLICATION NUMBER: PCT/US92/09752
 ATTORNEY/AGENT INFORMATION:
 NAME: COOPER, IVER P
 REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: ANDERSON=6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELX: 248633
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 ATTORNEY/AGENT INFORMATION:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ;
 ; US-08-443-890-21

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41
 RESULT 29
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41
 ;
 ; US-08-443-890-23
 ; Sequence 23, Application US/08443890
 ;
 ; Patient No. 5739011
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: ANDERSON, DAVID C.
 ; APPLICANT: MATHEWS, ANTONY JAMES
 ; APPLICANT: STETLER, GARY L.
 ; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC HEMOGLOBINS
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ;
 ; ADDRESSEE: Browdy and Neimark
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/443,890
 ; FILING DATE: 31-MAY-1995
 ; CLASSIFICATION: 530
 ;
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/240,712
 ; FILING DATE: 09-MAY-1994
 ; APPLICATION NUMBER: PCT/US92/09752
 ; FILING DATE: 13-MAY-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: COOPER, IVER P
 ; REGISTRATION NUMBER: 28,005
 ; REFERENCE/DOCKET NUMBER: ANDERSON=6
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELX: 248633
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 146 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ;
 ; US-08-443-890-22

RESULT 28
 ;
 ; Sequence 22, Application US/08443890
 ;
 ; Patient No. 5739011
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: ANDERSON, DAVID C.
 ; APPLICANT: MATHEWS, ANTONY JAMES
 ; APPLICANT: STETLER, GARY L.
 ; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC HEMOGLOBINS
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ;
 ; ADDRESSEE: Browdy and Neimark
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/443,890
 ; FILING DATE: 31-MAY-1995
 ; CLASSIFICATION: 530
 ;
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/240,712
 ; FILING DATE: 09-MAY-1994
 ; APPLICATION NUMBER: PCT/US92/09752
 ; FILING DATE: 13-MAY-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: COOPER, IVER P
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ;

REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: ANDERSON=6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

RESULT 30
 US-08-443-890-24
 ; Sequence 24, Application US/08443890
 ; Patent No. 5739011
 GENERAL INFORMATION:
 APPLICANT: ANDERSON, DAVID C.
 APPLICANT: MATHERS, ANTHONY JAMES
 APPLICANT: SETTLER, GARY L.
 TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
 TITLE OF INVENTION: HEMOGLOBINS
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brody and Neimark
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/443,890
 FILING DATE: 31-MAY-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/240,712
 FILING DATE: 09-MAY-1994
 APPLICATION NUMBER: PCT/US92/03752
 FILING DATE: 13-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: COOPER, IVER P
 REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: ANDERSON=6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

RESULT 31
 US-08-443-890-28
 ; Sequence 28, Application US/08443890
 ; Patent No. 5739011
 GENERAL INFORMATION:
 APPLICANT: ANDERSON, DAVID C.
 APPLICANT: MATHERS, ANTHONY JAMES
 APPLICANT: SETTLER, GARY L.
 TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
 TITLE OF INVENTION: HEMOGLOBINS
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brody and Neimark
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/443,890
 FILING DATE: 31-MAY-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/240,712
 FILING DATE: 09-MAY-1994
 APPLICATION NUMBER: PCT/US92/03752
 FILING DATE: 13-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: COOPER, IVER P
 REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: ANDERSON=6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

RESULT 32
 US-08-443-890-24
 ; Sequence 24, Application US/08443890
 ; Patent No. 5739011
 ; Sequence 28, Application US/08443890
 ; Patent No. 5739011
 ; Sequence 32, Application US/08443890
 ; Sequence 41, Application US/08443890

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,686B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/368,407
FILING DATE: 29-DEC-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/876,290
FILING DATE: 29-APR-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/684,511
FILING DATE: 12-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Flintoft, Gerald J.
REGISTRATION NUMBER: 20,823
REFERENCE/DOCKET NUMBER: 6666-043-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
;
US-08-484-686B-70
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
;
US-08-484-686B-68

Query Match 100 %; Score 10; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LVVWPWTQRF 10
||| |||||
Db 32 LVVWPWTQRF 41

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/684,611
FILING DATE: 12 APR 1991
ATTORNEY/AGENT INFORMATION:
NAME: Flintoff, Gerald J.
REGISTRATION NUMBER: 20,823
REFERENCE/DOCKET NUMBER: 6666-043-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANGENESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-686B-70

MOLECULE TYPE: protein
 DESCRIPTION: human -globin amino acid
 US-08-432-071B-4

Query Match 100.0%; Score 10; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 100.0%; Mismatches 0; Indels 0; Gaps 0;
 Sequence 10; Conservative 100.0%; Mismatches 0; Indels 0; Gaps 0;

RESULT 37
 US-08-627-173-18
 ; Sequence 18, Application US/08627173
 ; Patent No. 5861483
 GENERAL INFORMATION:
 APPLICANT: TSYRLOVA, IRENA
 APPLICANT: WOLPE, STEPHEN D.
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 TITLE OF INVENTION: USES THEREOF
 NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/627,173
 FILING DATE: 03-APR-1996
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/535,882
 FILING DATE: 28-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1331-177

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid

REFERENCE/DOCKET NUMBER: 1331-177

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid

STRANDEDNESS:
 TOPOLOGY: linear

MOLECULE TYPE: peptide
 US-08-627-173-22

Query Match 100.0%; Score 10; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 100.0%; Mismatches 0; Indels 0; Gaps 0;
 Sequence 10; Conservative 100.0%; Mismatches 0; Indels 0; Gaps 0;

RESULT 39
 US-08-482-920-10
 ; Sequence 10, Application US/08482920
 ; Patent No. 5861485
 GENERAL INFORMATION:
 APPLICANT: Donson, Jon
 APPLICANT: Dawson, William O.
 APPLICANT: Grantham, George L.
 APPLICANT: Turpen, Thomas H.
 APPLICANT: Turpen, Ann Myers
 APPLICANT: Garger, Stephen J.
 APPLICANT: Grill, Laurence K.
 TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
 NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,920
 FILING DATE: 07-JUNE-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 184,237
 FILING DATE: 19-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 600,244
 FILING DATE: 22-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 641,617
 FILING DATE: 16-JAN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 310,881
 FILING DATE: 17-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 160,766
 FILING DATE: 26-FEB-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 160,771
 FILING DATE: 05-MAY-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 363,138
 FILING DATE: 26-FEB-1988
 PRIOR APPLICATION DATA:
 REFERENCE/DOCKET NUMBER: 8129-112
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-854-3660
 TELEFAX: 415-854-3694
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-482-920-10

Query Match 100.0%; Score 10; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0;
 Matches 10; Conservative 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 41
 US-08-335-882A-22
 ; Sequence 22, Application US/08535882A.
 ; Patent No. 599391
 GENERAL INFORMATION:
 APPLICANT: TSYRLOVA, IRENA
 APPLICANT: WOLPE, STEPHEN D.
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERRHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/535,882A
 FILING DATE: 28-SEP-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REFERENCE/DOCKET NUMBER: 1331-177
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-535-882A-18

Query Match 100.0%; Score 10; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0;
 Matches 10; Conservative 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 40
 US-08-535-882A-18
 ; Sequence 18, Application US/08535882A.
 ; Patent No. 599391
 ; GENERAL INFORMATION:
 ; APPLICANT: TSYRLOVA, IRENA
 ; APPLICANT: WOLPE, STEPHEN D.
 ; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERRHYE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/535,882A
 FILING DATE: 28-SEP-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REFERENCE/DOCKET NUMBER: 1331-177
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEX: (703) 816-4000
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:

RESULT 42
 Query Match 100.0%; Score 10; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LVVYPTQRF 10
 |||||||
 Db 32 LVVYPTQRF 41

RESULT 42
 US-08-619-708A-6
 Sequence 6, Application US/08619708A
 Patent No. 5942488

GENERAL INFORMATION:
 APPLICANT: Komiyama, No. 5942488oru
 APPLICANT: Natai, Kyoshi
 TITLE OF INVENTION: Improvements In Or Relating To
 TITLE OF INVENTION: Haemoglobin
 NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Somatogen, Inc.
 STREET: 2545 Central Avenue, Suite F01
 CITY: Boulder
 STATE: Colorado
 ZIP: 80301

COMPUTER READABLE FORM:
 COMPUTER: Apple Macintosh, 3.50 inch, 1.4 Mb storage
 OPERATING SYSTEM: System 7.5
 SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/619,708A
 FILING DATE: 17 JUNE 1996
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB94/01996
 FILING DATE: 13 SEPT. 1994

ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Theresa A.
 REGISTRATION NUMBER: 32,547
 REFERENCE/DOCKET NUMBER: 280
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 816-4100
 TELEFAX: (303) 816-3356
 TELEFAX: 303-444-3013

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146
 TYPE: amino acid
 TOPOLOGY: unknown to applicant
 MOLECULE TYPE: protein
 HYPOTHETICAL: no

US-08-619-708A-6

RESULT 44
 US-08-316-424A-8
 Sequence 8, Application US/08316424A
 Patent No. 6022848

GENERAL INFORMATION:
 APPLICANT: KOZLOV, VLADIMIR
 APPLICANT: TSYRLOVA, IRINA
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 USES THEREOF
 NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P. C.
 STREET: 1100 NORTH GLBEE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

RESULT 43
 US-08-316-424A-4

Best Local Similarity 100.0%; Pred. No. 0.00018; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYWTQRF 10
Db 32 LVVYWTQRF 41

RESULT 47
US-08-484-341-10
Sequence 10; Application US/08484341
GENERAL INFORMATION:
APPLICANT: Donson, Jon
Dawson, William O.
Graham, George L.
Turpen, Thomas H.
Turpen, Ann Myers
Garrer, Stephen J.
Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Farry Building
CITY: San Francisco
STATE: CA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484.341
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184, 237
FILING DATE: <Unknown>
APPLICATION NUMBER: US 500, 244
FILING DATE: 22-Oct-1990
APPLICATION NUMBER: US 641, 617
FILING DATE: 16-Jan-1991
APPLICATION NUMBER: US 310, 881
FILING DATE: 17-Feb-1989
APPLICATION NUMBER: US 160, 766
FILING DATE: 26-Feb-1988
APPLICATION NUMBER: US 160, 771
FILING DATE: 05-May-1989
APPLICATION NUMBER: US 363, 138
FILING DATE: 08-Jun-1989
APPLICATION NUMBER: US 219, 279
FILING DATE: 15-Jul-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halulin, Albert P.
REGISTRATION NUMBER: 28, 957
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-484-341-10

RESULT 48
US-09-005-546-18
Sequence 18; Application US/09005546
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
PATENT NO. 6090782
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005, 546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535, 882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32, 205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-005-546-18

Query Match 100.0%; Score 10; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYWTQRF 10
Db 32 LVVYWTQRF 41

RESULT 49
US-09-005-546-22
Sequence 22; Application US/09005546
GENERAL INFORMATION:
PATENT NO. 6090782
APPLICANT: TSYRLOVA, IRENA
APPLICANT: WOLPE, STEPHEN D.
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND USES THEREOF
NUMBER OF SEQUENCES: 27

Query Match 100.0%; Score 10; DB 3; Length 146;

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/005,546

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/535,882

FILING DATE: 28-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 1331-177

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4100

TELEFAX: (703) 816-4000

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 146 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-09-005-546-22

QY 1 LVVYPWTFQRF 10
|||||||
Db 32 LVVYPWTFQRF 41RESULT 51
US-09-230-603-12
Sequence 12, Application US/09230603
; Sequence 12, Application US/09230603
; Patent No. 6171826QY 1 LVVYPWTFQRF 10
|||||||
Db 32 LVVYPWTFQRF 41Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;

RESULT 53

US-09-230-603-17

; Sequence 17, Application US/09230603

; Patent No. 6171826

GENERAL INFORMATION:

APPLICANT: APOSTOL, IZYDOR A

APPLICANT: LEVINE, JOSEPH D

TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN

FILE REFERENCE: BXTB3060

CURRENT APPLICATION NUMBER: US/09/230,603

CURRENT FILING DATE: 1999-05-14

EARLIER APPLICATION NUMBER: PCT/US97/113564

EARLIER FILING DATE: 1997-08-01

EARLIER FILING DATE: 1996-08-02

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 17

LENGTH: 146

TYPE: PRT

ORGANISM: Escherichia coli

US-09-230-603-17

Db 3 : LVVYPTQRF 42

RESULT 55

US-08-463-160B-67

; Sequence 67, Application US/08463160B

; Patent No. 6172039

GENERAL INFORMATION:

APPLICANT: De Angelo, Joseph

APPLICANT: Motwani, Nalini

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HEMOGLOBIN

TITLE OF INVENTION: AND HEMOGLOBIN VARIANTS IN YEAST

NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:

ADRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDİUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,160B

FILING DATE: 05-JUN-1995

CLASIFICATION: 530

PRICR APPLICATION DATA:

APPLICATION NUMBER: US 08/368,407

FILING DATE: 29-DEC-1994

PRICR APPLICATION DATA:

APPLICATION NUMBER: US 07/876,290

FILING DATE: 29-APR-1992

PRICR APPLICATION DATA:

APPLICATION NUMBER: US 07/684,611

FILING DATE: 12-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Flintoft, Gerald J.

REGISTRATION NUMBER: 20,823

REFERENCE/DOCKET NUMBER: 6666-044-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 146 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-463-160B-67

RESULT 56

US-08-463-160B-68

; Sequence 68, Application US/08463160B

; Patent No. 6172039

GENERAL INFORMATION:

APPLICANT: De Angelis, Joseph

APPLICANT: Motwani, Nalini

Query Match 100.0%; Score 10; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10
 Db 32 LVVYPTQRF 41

RESULT 53
 US-09-230-603-17
 ; Sequence 17, Application US/09230603
 ; Patent No. 6171826
 GENERAL INFORMATION:
 APPLICANT: APOSTOL, IZYDOR A
 APPLICANT: LEVINE, JOSEPH D
 TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
 FILE REFERENCE: BXTB3060
 CURRENT APPLICATION NUMBER: US/09/230,603
 CURRENT FILING DATE: 1999-05-14
 EARLIER APPLICATION NUMBER: PCT/US97/113564
 EARLIER FILING DATE: 1997-08-01
 EARLIER FILING DATE: 1996-08-02
 NUMBER OF SEQ ID NOS: 22
 SEQ ID NO 17
 LENGTH: 146
 TYPE: PRT
 ORGANISM: Escherichia coli
 FEATURE:
 NAME/KEY: NON_TER
 LOCATION: (1)
 OTHER INFORMATION: the N-terminal methionine residue incorporated during the translation initiation step is excised
 OTHER INFORMATION: during translation and is not present in the other information
 OTHER INFORMATION: mature polypeptide chain
 US-09-230-603-20

Query Match 100.0%; Score 10; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10
 Db 32 LVVYPTQRF 41

RESULT 55
 US-08-463-160B-67
 ; Sequence 67, Application US/08463160B
 ; Patent No. 6172039
 GENERAL INFORMATION:
 APPLICANT: De Angelo, Joseph
 APPLICANT: Motwani, Nalini

Query Match 100.0%; Score 10; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10
 Db 32 LVVYPTQRF 41

RESULT 56
 US-08-463-160B-68
 ; Sequence 68, Application US/08463160B
 ; Patent No. 6172039
 GENERAL INFORMATION:
 APPLICANT: De Angelis, Joseph
 APPLICANT: Motwani, Nalini

APPLICANT: Bajwa, Waheed
 TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HEMOGLOBIN
 NUMBER OF SEQUENCES: 71
 CORRESPONDENCE ADDRESS:
 STREET: 115 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,160B

FILING DATE: 05-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/368,407

FILING DATE: 29-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/876,290

FILING DATE: 29-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/684,611

FILING DATE: 12-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/684,611

FILING DATE: 12-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/823

FILING DATE: 29-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/876,290

FILING DATE: 29-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/684,611

FILING DATE: 12-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/684,611

FILING DATE: 12-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/684,611

FILING DATE: 12-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/684,611

FILING DATE: 12-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/684,611

FILING DATE: 12-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/684,611

FILING DATE: 12-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/684,611

FILING DATE: 12-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/684,611

FILING DATE: 12-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/684,611

FILING DATE: 12-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/684,611

FILING DATE: 12-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/684,611

FILING DATE: 12-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/684,611

FILING DATE: 12-APR-1991

Query Match 100.0%; Score 10; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Type: amino acid

QY 1 LVVVPWTFR 10
 |||||||
 Db 32 LVVVPWTFR 41

RESULT 58
 US-08-463-160B-71
 Sequence 71, Application US/08463160B
 Patent No. 6172039

GENERAL INFORMATION:
 APPLICANT: De Angelo, Joseph
 APPLICANT: Motwani, Nalini

APPLICANT: Bajwa, Waheed
 APPLICANT: Motwani, Nalini
 TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HEMOGLOBIN
 NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 115 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/463,160B
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/368,407
 FILING DATE: 29-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/876,290
 FILING DATE: 29-APR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/684,611
 FILING DATE: 12-APR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Flintoft, Gerald J.
 REGISTRATION NUMBER: 20,823
 REFERENCE/DOCKET NUMBER: 6666-044-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 MOLECULE TYPE: Peptide
 US-08-463-160B-71

Query Match 100.0%; Score 10; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTFQE 10
 Db 32 LVVYPWTFQE 41

RESULT 59
 US-09-058-562-19
 Sequence 19, Application US/09058562A
 Patent No. 6184356
 GENERAL INFORMATION:
 APPLICANT: Anderson, David C.
 APPLICANT: Mathews, Antony James
 APPLICANT: Stetler, Gary L.

Query Match 100.0%; Score 10; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTFQE 10
 Db 32 LVVYPWTFQE 41

RESULT 51
 US-09-053-562-22
 Sequence 22, Application US/09058562A
 Patent No. 6184356
 GENERAL INFORMATION:
 APPLICANT: Anderson, David C.
 APPLICANT: Mathews, Antony James
 APPLICANT: Stetler, Gary L.

Query Match 100.0%; Score 10; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTFQE 10
 Db 32 LVVYPWTFQE 41

RESULT 51
 US-09-053-562-22
 Sequence 22, Application US/09058562A
 Patent No. 6184356
 GENERAL INFORMATION:
 APPLICANT: Anderson, David C.
 APPLICANT: Mathews, Antony James
 APPLICANT: Stetler, Gary L.

Query Match 100.0%; Score 10; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTFQE 10
 Db 32 LVVYPWTFQE 41

RESULT 51
 US-09-053-562-22
 Sequence 22, Application US/09058562A
 Patent No. 6184356
 GENERAL INFORMATION:
 APPLICANT: Anderson, David C.
 APPLICANT: Mathews, Antony James
 APPLICANT: Stetler, Gary L.

Query Match 100.0%; Score 10; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTFQE 10
 Db 32 LVVYPWTFQE 41

RESULT 62
 US-09-058-562-26
 Sequence 26, Application US/09058562A
 Patent No. 6184356
 GENERAL INFORMATION:
 APPLICANT: Anderson, David C.
 APPLICANT: Mathews, Antony James
 APPLICANT: Stetler, Gary L.

Query Match 100.0%; Score 10; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTFQE 10
 Db 32 LVVYPWTFQE 41

RESULT 60
 US-09-058-562-20
 Sequence 20, Application US/09058562A

TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC HEMOGLOBINS

FILE REFERENCE: BYTB 2087

CURRENT APPLICATION NUMBER: US/09/058,52A

CURRENT FILING DATE: 1998-04-13

PRIOR APPLICATION NUMBER: US 08/240,712

PRIOR FILING DATE: 1994-05-09

PRIOR APPLICATION NUMBER: PCT/US92/09752

PRIOR FILING DATE: 1993-05-13

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO: 26

LENGTH: 146

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: beta globin

US-09-058-562-26

RESULT 63
US 09-031-361-2
Sequence 2, Application US/09031361
; Patent No. 6204009
; GENERAL INFORMATION:
; APPLICANT: Olson, John S.
; APPLICANT: Mathews, Antony J.
; APPLICANT: Aitken, Jacqueline F.
; APPLICANT: Nagai, Kiyoshi
TITLE OF INVENTION: Mutant Recombinant Hemoglobins
TITLE OF INVENTION: Containing Heme Pocket Mutations
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Somatogen, Inc.
STREET: 2245 Central Avenue, Suite F01
CITY: Boulder
STATE: Colorado
ZIP: 80301

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,361
FILING DATE: 26-FEB-1998
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/381,175
FILING DATE: 30-JAN-1995
APPLICATION NUMBER: 08/158,483
FILING DATE: 29-NOV-1993
APPLICATION NUMBER: 07/443,950
FILING DATE: 12-DEC-1998
APPLICATION NUMBER: 07/104,338
FILING DATE: 16-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Theresa A.
REGISTRATION NUMBER: 32547
REFERENCE/DOCKET NUMBER: 221 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3324
TELEFAX: 303-444-3013
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 146

TYPE: amino acid

TOPOLOGY: unknown to applicant

MOLECULE TYPE: protein

HYPOTHETICAL: no

US-09-031-361-2

RESULT 64
US-08-483-502-10
; Sequence 10, Application US/08483502
; Patent No. 6284492
; GENERAL INFORMATION:
; APPLICANT: Donson, Jon
; APPLICANT: Dawson, William O.
; APPLICANT: Grantham, George L.
; APPLICANT: Turpen, Thomas H.
; APPLICANT: Turpen, Ann Myers
; APPLICANT: Garger, Stephen J.
; APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,502
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/739,143
FILING DATE: 16-JAN-1991
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 219,279

FILING DATE: 15-JUL-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Innen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 18604-090574
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 TELEX: 202-962-8300
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-483-502-10

Query Match 100.0%; Score 10; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Gaps 0;
 Qy 1 LVVYPWQRF 10
 Db 32 LVVYPWQRF 41

RESULT 65

US-09-352-078-1

Sequence 1, Application US/09352078

PATENT INFORMATION:

APPLICANT: Theragen, Inc.
 APPLICANT: Hoffman, Brian F.
 APPLICANT: Dubnick, Bernard
 TITLE OF INVENTION: USE OF MAMMALIAN-DERIVED PEPTIDES FOR
 TREATMENT OF MICROBIAL INFECTIONS
 FILE REFERENCE: 1144/1B0990S1
 CURRENT APPLICATION NUMBER: US/09/352,078
 EARLIER APPLICATION NUMBER: PCT/US98/16746
 EARLIER FILING DATE: 1998-08-10
 EARLIER APPLICATION NUMBER: 60/061,454
 EARLIER FILING DATE: 1997-10-08
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 146
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-352-078-1
 Sequence 1, Application US/09352078
 PATENT INFORMATION:
 APPLICANT: Theragen, Inc.
 APPLICANT: Hoffman, Brian F.
 APPLICANT: Dubnick, Bernard
 TITLE OF INVENTION: USE OF MAMMALIAN-DERIVED PEPTIDES FOR
 TREATMENT OF MICROBIAL INFECTIONS
 FILE REFERENCE: 1144/1B0990S1
 CURRENT APPLICATION NUMBER: US/09/352,078
 EARLIER APPLICATION NUMBER: PCT/US98/16746
 EARLIER FILING DATE: 1998-08-10
 EARLIER APPLICATION NUMBER: 60/061,454
 EARLIER FILING DATE: 1997-10-08
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 146
 TYPE: PRT
 ORGANISM: Homo sapiens

Query Match 100.0%; Score 10; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Gaps 0;
 Qy 1 LVVYPWQRF 10
 Db 32 LVVYPWQRF 41

RESULT 67

PC/TUS2-09752-19

Sequence 19, Application PC/TUS9209752

GENERAL INFORMATION:

APPLICANT: ANDERSON, DAVID C.
 APPLICANT: MATHEWS, ANTHONY JAMES
 APPLICANT: STELLER, GARRY L.
 TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
 HEMOGLOBINS
 NUMBER OF SEQ ID NOS: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Browdy and Neimark
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004

COMPUTER READABLE FORM:
 COMPUTER TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/09752
 FILING DATE: 19930109
 CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
 NAME: COOPER, IVER P
 REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: ANDERSON-6-PCT

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633

INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US92-09752-19

Query Match 100.0%; Score 10; DB 5; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10
Db 32 LVVYPWTORF 41

RESULT 68
PCT-US92-09752-20
; Sequence 20, Application PC/TUS9209752
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DAVID C.
; APPLICANT: MATHEWS, ANTONY JAMES
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09752
; FILING DATE: 19930109
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: ANDERSON-6-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US92/09752-21

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-09752-20

RESULT 70
PCT-US92-09752-22
; Sequence 22, Application PC/TUS9209752
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DAVID C.
; APPLICANT: MATHEWS, ANTONY JAMES
; APPLICANT: STELTER, GARY L.
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09752
; FILING DATE: 19930109
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: ANDERSON-6-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197

Query Match 100.0%; Score 10; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVYPWTORF 10
Db 32 LVVYPWTORF 41

RESULT 69
PCT-US92-09752-21
; Sequence 21, Application PC/TUS9209752
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DAVID C.
; APPLICANT: MATHEWS, ANTONY JAMES
; APPLICANT: STELTER, GARY L.
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark

TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US92-09752-22

Query Match 100.0%; Score 10; DB 5; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; MisMatches 0; Del 0; Insert 0;

Qy 1 LVVYPWTRF 10
 Db 32 LVVYPWTRF 41

RESULT ?1
 PCT-US92-09752-23

; Sequence 23, Application PC/TUS9209752
 ; GENERAL INFORMATION:
 ; APPLICANT: ANDERSON, DAVID C.
 ; APPLICANT: MATHERS, ANTONY JAMES
 ; APPLICANT: STETLER, GARY L.
 ; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Browdy and Neimark
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT-US92/09752
 FILING DATE: 19930109
 CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
 NAME: COOPER, IVER P
 REGISTRATION NUMBER: 28 005

REFERENCE/DOCKET NUMBER: ANDERSON-6-PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528
 TELE: 248633

INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US92-09752-24

Query Match 100.0%; Score 10; DB 5; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; MisMatches 0; Del 0; Insert 0;

Qy 1 LVVYPWTRF 10
 Db 32 LVVYPWTRF 41

RESULT ?2
 PCT-US92-09752-24

; Sequence 24, Application PC/TUS9209752
 ; GENERAL INFORMATION:
 ; APPLICANT: ANDERSON, DAVID C.
 ; APPLICANT: MATHERS, ANTONY JAMES
 ; APPLICANT: STETLER, GARY L.
 ; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Browdy and Neimark
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT-US92/09752
 FILING DATE: 19930109
 CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
 NAME: COOPER, IVER P
 REGISTRATION NUMBER: 28 005

REFERENCE/DOCKET NUMBER: ANDERSON-6-PCT

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528
 TELE: 248633

INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US92-09752-23

Query Match 100.0%; Score 10; DB 5; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; MisMatches 0; Del 0; Insert 0;

Qy 1 LVVYPWTRF 10
 Db 32 LVVYPWTRF 41

RESULT ?3
 PCT-US92-09752-28

; Sequence 28, Application PC/TUS9209752
 ; GENERAL INFORMATION:

; APPLICANT: ANDERSON, DAVID C.
 ; APPLICANT: MATHERS, ANTONY JAMES
 ; APPLICANT: STETLER, GARY L.
 ; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Browdy and Neimark
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004

COMPUTER READABLE FORM:
 COMPUTER: Floppy disk

TYPE: PRT
 ORGANISM: Escherichia coli
 FEATURE:
 NAME/KEY: NON_TER
 LOCATION: (1)
 OTHER INFORMATION: the N-terminal methionine residue incorporated during the translation initiation step is excised
 OTHER INFORMATION: during the translation and is not present in the other information
 OTHER INFORMATION: mature polypeptide chain
 US-09-230-603-15

Query Match 100.0%; Score 10; DB 4; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVVPWTQRF 10
 Db 33 LVVVPWTQRF 42

RESULT 77
 US-09-230-603-16
 ; Sequence 16, Application US/09230603
 ; Patent No. 6171826
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, JOSEPH D
 ; TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
 ; TITLE OF INVENTION: HEMOGLOBIN
 ; FILE REFERENCE: BXTB060
 ; CURRENT APPLICATION NUMBER: US/09/230, 603
 ; CURRENT FILING DATE: 1999-05-14
 ; EARLIER APPLICATION NUMBER: PCT/US97/13564
 ; EARLIER FILING DATE: 1997-08-01
 ; EARLIER APPLICATION NUMBER: 60/023, 211
 ; EARLIER FILING DATE: 1996-08-02
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 16
 ; LENGTH: 147
 ; TYPE: PRT
 ; FEATURE:
 ; ORGANISM: Escherichia coli
 ; NAME/KEY: NON_TER
 ; LOCATION: (1)
 ; OTHER INFORMATION: the N-terminal methionine residue incorporated during the translation initiation step is excised
 ; OTHER INFORMATION: during the translation and is not present in the other information
 ; OTHER INFORMATION: mature polypeptide chain
 US-09-230-603-16

Query Match 100.0%; Score 10; DB 4; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVVPWTQRF 10
 Db 33 LVVVPWTQRF 42

RESULT 79
 US-09-230-603-19
 ; Sequence 19, Application US/09230603
 ; Patent No. 6171826
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, JOSEPH D
 ; TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
 ; TITLE OF INVENTION: HEMOGLOBIN
 ; FILE REFERENCE: BXTB060
 ; CURRENT APPLICATION NUMBER: US/09/230, 603
 ; CURRENT FILING DATE: 1999-05-14
 ; EARLIER APPLICATION NUMBER: PCT/US97/13564
 ; EARLIER FILING DATE: 1997-08-01
 ; EARLIER APPLICATION NUMBER: 60/023, 211
 ; EARLIER FILING DATE: 1996-08-02
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.1.
 ; SEQ ID NO: 19
 ; LENGTH: 147
 ; TYPE: PRT
 ; FEATURE:
 ; ORGANISM: Escherichia coli
 ; NAME/KEY: NON_TER
 ; LOCATION: (1)
 ; OTHER INFORMATION: the N-terminal methionine residue incorporated during the translation initiation step is excised
 ; OTHER INFORMATION: during the translation and is not present in the other information
 ; OTHER INFORMATION: mature polypeptide chain
 US-09-230-603-19

Query Match 100.0%; Score 10; DB 4; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVVPWTQRF 10
 Db 33 LVVVPWTQRF 42

RESULT 78
 US-09-230-603-18
 ; Sequence 18, Application US/09230603
 ; Patent No. 6171826
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, JOSEPH D
 ; APPLICANT: APOSTOL, IZYDOR A
 ; TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
 ; TITLE OF INVENTION: HEMOGLOBIN
 ; FILE REFERENCE: BXB3060
 ; CURRENT APPLICATION NUMBER: US/09/230, 603

Query Match 100.0%; Score 10; DB 4; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVVPWTQRF 10
 Db 33 LVVVPWTQRF 42

RESULT 80
 US-09-058-562-21

Sequence 21, Application US/09058562A
 PATENT NO. 6184356
 GENERAL INFORMATION:

APPLICANT: Anderson, David C.
 APPLICANT: Mathews, Antony James

TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC HEMOGLOBINS
 FILE REFERENCE: BXTB 2087
 CURRENT APPLICATION NUMBER: US/09/058 562A
 CURRENT FILING DATE: 1998-04-13
 PRIOR APPLICATION NUMBER: US 08/240,712
 PRIOR FILING DATE: 1993-05-13
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 21

LENGTH: 147
 TYPE: PRY
 ORGANISM: Human hemoglobin

FEATURE: VARIANT
 NAME/KEY: VARIANT
 LOCATION: (75)

OTHER INFORMATION: Xaa= Ile or Thr
 US-09-058-562-21

RESULT 81

US-08-627-173-5
 Sequence 5, Application US/08627173
 Patent No. 5861483
 GENERAL INFORMATION:

APPLICANT: TSYRIOVA, IRENA
 APPLICANT: WOLPE, STEPHEN D.
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 TITLE OF INVENTION: USES THEREOF
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/535,882A
 FILING DATE: 28-SEP-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1331-177

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: linear
 MOLECULE TYPE: peptide

US-08-535-882A-5

Query Match 100.0%; Score 10; DB 4; Length 147;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 81
 US-08-627-173-5
 Sequence 5, Application US/08627173
 Patent No. 5861483
 GENERAL INFORMATION:
 APPLICANT: TSYRIOVA, IRENA
 APPLICANT: WOLPE, STEPHEN D.
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 TITLE OF INVENTION: USES THEREOF
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/535,882A
 FILING DATE: 28-SEP-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1331-177

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: linear
 MOLECULE TYPE: peptide

US-08-535-882A-5

Query Match 90.0%; Score 9; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTQRF 9
 Db 1 LVVYPWTQRF 9

RESULT 83
 US-09-005-546-5
 Sequence 5, Application US/09005546

PATENT NO. 6090782
 GENERAL INFORMATION:
 APPLICANT: TSYRLOVA, IRENA
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/005,546
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/535,882
 FILING DATE: 28-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REFERENCE NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1331-177
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide
 US-09-005-546-5

Query Match 90.0%; Score 9; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQR 9
 Db 1 LVVYPWTQR 9

RESULT 85
 US-08-535-882A-20
 Sequence 20, Application US/08535882A
 Patent No. 593931
 GENERAL INFORMATION:
 APPLICANT: TSYRLOVA, IRENA
 APPLICANT: WOLPE, STEPHEN D.
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/535,882A
 FILING DATE: 28-SEP-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REFERENCE NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1331-177
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear

US-09-005-546-5

RESULT 84
 US-08-627-173-20
 Sequence 20, Application US/08627173
 Patent No. 5861483
 GENERAL INFORMATION:
 APPLICANT: TSYRLOVA, IRENA
 APPLICANT: WOLPE, STEPHEN D.
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/535,882A
 FILING DATE: 28-SEP-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REFERENCE NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1331-177
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear

US-08-627-173-20

; MOLECULE TYPE: peptide
; US-08-535-882A-20

Query Match 90.0%; Score 9; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0022; Mismatches 0;
Matches 9; Conservative 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQR 9
Db 32 LVVYPWTQR 40

RESULT 86

; Sequence 6, Application US/08316424A

; PATENT NO. 6022848

; GENERAL INFORMATION:

; APPLICANT: KOZLOV, VLADIMIR

; INVENTOR: TSYRLOVA, IRENA

; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, version #1.30

; CURRENT APPLICATION DATA:

; FILING DATE: 30-SEP-1994

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/535, 882

; FILING DATE: 28-SEP-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: BYRNE, THOMAS E.

; REFERENCE/DOCKET NUMBER: 1331-122

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 146 amino acids

; STRANDEDNESS:

; TOPOLOGY: linear

; INFORMATION FOR SEQ ID NO: 6:

; MOLECULE TYPE: peptide

; US-08-316-424A-6

RESULT 87

US-09-005-546-20

; Sequence 6, Application US/08005546

; Patent No. 6090782

; GENERAL INFORMATION:

; APPLICANT: TSYRLOVA, IRENA

; INVENTOR: WOLPE, STEPHEN D.

; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, version #1.30

; CURRENT APPLICATION DATA:

; FILING DATE: 01-APR-1996

; CLASSIFICATION: 514

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/535,882

FILING DATE: 28-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REFERENCE/DOCKET NUMBER: 32,205

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-627-173-6

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-627-173-27

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-627-173-177

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-627-173-177

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-627-173-177

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-627-173-177

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-627-173-177

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-627-173-177

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-627-173-177

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-627-173-177

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-627-173-177

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

RESULT 89

SEQUENCE 27, Application US/08627173

Patient No. 5861483

GENERAL INFORMATION:

APPLICANT: TSRLOVA, IRENA

TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND USES THEREOF

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLBRE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/535,882A

FILING DATE: 28-SEP-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 1331-177

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

RESULT 91

SEQUENCE 27, Application US/08535882A

Patient No. 5939391

GENERAL INFORMATION:

APPLICANT: TSRLOVA, IRENA

TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND USES THEREOF

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.

ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/535,882A
 FILING DATE: 28-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.

ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1331-177
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ; US-09-005-546-6

INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 ; US-08-535-882A-27

Query Match 92
 Best Local Similarity 100.0%; Score 8; DB 2; Length 8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 WWPWTQ 9
 Db 1 WWPWTQ 8

Query Match 80.0%
 Best Local Similarity 100.0%; Score 8; DB 3; Length 8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 WWPWTQ 9
 Db 1 WWPWTQ 8

Query Match 93
 Best Local Similarity 100.0%; Score 8; DB 3; Length 8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LUVYPWTQ 8
 Db 1 LUVYPWTQ 8

Query Match 93
 Best Local Similarity 100.0%; Score 8; DB 3; Length 8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LUVYPWTQ 8
 Db 1 LUVYPWTQ 8

RESULT 92
 US-09-005-546-6
 Sequence 6, Application US/09005546
 Patient No. 6090782
 GENERAL INFORMATION:
 APPLICANT: TSYRLOVA, IRENA
 ADDRESS: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/005,546
 FILING DATE: 28-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1331-177
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ; US-09-005-546-6

Query Match 80.0%
 Best Local Similarity 100.0%; Score 8; DB 3; Length 8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 94
QY 2 VVYPWTQ 9
|||
US-08-627-173-7
; Sequence 7, Application US/08627173
; Patent No. 5861483
; GENERAL INFORMATION:
; APPLICANT: TSYRLOVA, IRENA
; APPLICANT: WOLPE, STEPHEN D.
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERRHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,173
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,882
; FILING DATE: 28-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1331-177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; FAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-627-173-10
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-627-173-7
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-627-173-7
Query Match 70.0%; score 7; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVWVPT 7
|||
Db 1 LVWVPT 7
; RESULT 95
; US-08-627-173-10
; Sequence 10, Application US/08627173
; Patent No. 5861483
; GENERAL INFORMATION:
; APPLICANT: TSYRLOVA, IRENA
; APPLICANT: WOLPE, STEPHEN D.
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERRHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,173
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,882
; FILING DATE: 28-SEP-1995
; ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1331-177
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

Query Match 70.0% Score 7; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YPWNQRF 10
 Db 1 YPWNQRF 7

RESULT 97
 US-08-535-882A-7
 Sequence 7, Application US/08535882A
 ; Patent No. 5939391
 ; GENERAL INFORMATION:
 APPLICANT: TSYRLOVA, IRENA
 APPLICANT: WOLPE, STEPHEN D.
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 TITLE OF INVENTION: USES THEREOF
 NUMBER OF SEQUENCES: 27
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHIVE P. C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

COMPUTER READABLE FORM:
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/535,882A
 FILING DATE: 28-SEP-1995

ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 CLASSIFICATION: 435

REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1331-177
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-535-882A-10
 Query Match 70.0% Score 7; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 WVWPWTQ 8
 Db 1 WVWPWTQ 7

RESULT 99
 US-08-535-882A-11
 Sequence 11, Application US/08535882A
 ; Patent No. 5939391
 ; GENERAL INFORMATION:
 APPLICANT: TSYRLOVA, IRENA
 APPLICANT: WOLPE, STEPHEN D.
 TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 TITLE OF INVENTION: USES THEREOF
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHIVE P. C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

Query Match 70.0% Score 7; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNVVWPWT 7

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-08/535,882A
 FILING DATE: 28-SEP-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1331-177
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-535-882A-11

Query Match 70.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPWTQRF 10
 Db 1 YPWTQRF 7

RESULT 100

US-08-981-384-1
 Sequence 1, Application US/08981384
 Patent No. 6046168
 GENERAL INFORMATION:
 APPLICANT: Kogawa, Kyōichi
 APPLICANT: Fukuhama, Chizuko
 APPLICANT: Matsutaka, Hisako
 APPLICANT: Nakamura, Toyoo
 APPLICANT: Numata, Masahiro
 APPLICANT: Watanabe, Shigeaki
 APPLICANT: Honda, Kazuhisa
 TITLE OF INVENTION: A peptide inhibiting elevations of triglycerides in blood and an agent for inhibiting elevations of triglycerides in blood comprising the peptide as title of invention; an active component
 FILE REFERENCE: 382,1016
 CURRENT APPLICATION NUMBER: US/08/981,384
 CURRENT FILING DATE: 1997-12-23
 EARLIER APPLICATION NUMBER: PCT/JP95/01264
 EARLIER FILING DATE: 1995-06-23
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 7
 TYPE: PRY
 ORGANISM: Bos frontalis
 US-08-981-384-1

Search completed: July 1, 2002, 12:06:49
 Job time: 22 sec

Query	Match	Score	DB	Length
QY 1	LWVYPWT	7	3	7
Db 1	LWVYPWT	7		

Best Local Similarity 100.0%; Pred. No. 1.7e+05; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue Jul 2 09:03:46 2002

us-09-147-490-1.rai

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ALIGNMENTS

R; Cleary, M.L.; Schon, E.A.; Lingrel, J.B.
Cell 26, 181-190, 1981

RESULT 1
165317
hemoglobin delta chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Jul-1996 #sequence_revision 31-Jul-1997 #text_change 20-Apr-2000
C;Accession: 165317
R;Liu, J.Z.; Marano, T.; Lancios, K.D.; Huisman, T.H.
Biophys. Acta 909, 208-212, 1987
A;Title: The beta-delta crossover leading to the beta delta hybrid gene of hemoglobin P-
A;Reference number: 152502; MUID:87299720
A;Accession: I65317
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-110 <CDE>
A;Cross-references: EMBL:V00154; NID:9965; PIDN:CAA23469.1; PID:9966
A;Genetics:
A;Gene: GDB:HBD
A;Cross-references: GDB:119298
A;Map position: 11p15.5-11p15.5
A;Introns: 31/3

Query Match 100.0%; Score 10; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 9e-05; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 31-Jul-1997 #text_change 20-Apr-2000
C;Accession: 152502
R;Liu, J.Z.; Marano, T.; Lancios, K.D.; Huisman, T.H.
Biophys. Acta 909, 208-212, 1987
A;Title: The beta-delta crossover leading to the beta delta hybrid gene of hemoglobin P-
A;Reference number: 152502; MUID:87299720
A;Accession: I52502
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-61 <LIU>
A;Cross-references: GB:M25660; PIDN:AAA53153.1; PID:9183857
A;Note: this sequence was not determined in this report
C;Genetics:
A;Gene: GDB:HBD
A;Cross-references: GDB:119297
A;Map position: 11p15.4-11p15.4
A;Introns: 31/3

RESULT 2
152502
hemoglobin beta chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 31-Jul-1997 #text_change 20-Apr-2000
C;Accession: 152502
R;Liu, J.Z.; Marano, T.; Lancios, K.D.; Huisman, T.H.
Biophys. Acta 909, 208-212, 1987
A;Title: The beta-delta crossover leading to the beta delta hybrid gene of hemoglobin P-
A;Reference number: 152502; MUID:87299720
A;Accession: I52502
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-122 <NAQ>
A;Note: the peptides were positioned by homology
C;Superfamily: globin; globin homology
C;Keywords: Chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F;3-122/Domain: globin homology (fragments) <GB>
F;80/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.00015; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 31-Jul-1997 #text_change 20-Apr-2000
C;Accession: 152502
R;Liu, J.Z.; Marano, T.; Lancios, K.D.; Huisman, T.H.
Biophys. Acta 909, 208-212, 1987
A;Title: The beta-delta crossover leading to the beta delta hybrid gene of hemoglobin P-
A;Reference number: 152502; MUID:87299720
A;Accession: I52502
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-122 <NAQ>
A;Cross-references: GB:M25660; PIDN:AAA53153.1; PID:9183857
A;Note: this sequence was not determined in this report
C;Genetics:
A;Gene: GDB:HBD
A;Cross-references: GDB:119297
A;Map position: 11p15.4-11p15.4
A;Introns: 31/3

RESULT 3
1 LVVYPWTQRF 10
Db 33 LVVYPWTQRF 42

Query Match 100.0%; Score 10; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 9e-05; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 21-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 19-May-2000
C;Accession: I46172
A;Title: hypothetical hemoglobin psi-beta-z pseudogene - goat (fragment)
A;Species: Capra aegagrus hircus (domestic goat)
C;Date: 21-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 19-May-2000
C;Accession: I46172
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA

R; Cleary, M.L.; Schon, E.A.; Lingrel, J.B.
Cell 26, 181-190, 1981
A;Title: Two related pseudogenes are the result of a gene duplication in the goat bet cell
A;Reference number: I46172; MUID:82137052
A;Accession: 146172
A;Title: Two related pseudogenes are the result of a gene duplication in the goat bet cell
A;Molecule type: DNA
A;Residues: 1-110 <CDE>
A;Cross-references: EMBL:V00154; NID:9965; PIDN:CAA23469.1; PID:9966
A;Genetics:
A;Introns: 11/3; 18/3; 29/2; 103/3
C;Keywords: pseudogene

Query Match 100.0%; Score 10; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.00014; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C;Species: Uromastyx hardwickii (Indian spiny-tailed lizard)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
C;Accession: A05304
R;Aqvi, S.; Zaidi, Z.H.; von Bahr-Lindstrom, H.; Carlquist, M.; Jornvall, H.
FEBS Lett. 162, 290-295, 1983
A;Reference number: A91314; MUID:84029159
A;Accession: A05304
A;Molecule type: protein
A;Residues: 1-122 <NAQ>
A;Note: the peptides were positioned by homology
C;Superfamily: globin; globin homology
C;Keywords: Chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F;3-122/Domain: globin homology (fragments) <GB>
F;80/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.00015; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 03-Mar-2000
C;Accession: B02396; I46277; A02396
R;Schon, E.A.; Cleary, M.L.; Haynes, J.R.; Lingrel, J.B.
Cell 27, 359-369, 1981
A;Title: Structure and evolution of goat gamma-, beta(c)- and beta(A)-globin genes: t
A;Reference number: A90817; MUID:82137075
A;Accession: B02396
A;Molecule type: DNA
A;Residues: 1-141 <SCH>
A;Cross-references: GB:M15389
A;Note: Initiator Met not shown
R;Haynes, J.R.; Rostock, P.R.; Schon, E.A.; Gallagher, P.M.; Burks, D.J.; Smith, K.;
J. Biol. Chem. 255, 6355-6367, 1980
A;Title: The isolation of the beta-a-, beta-c-, and gamma-globin genes and a presumpt
A;Reference number: I46273; MUID:80227766
A;Accession: I46277
A;Status: preliminary; translated from GB/EMBL/DDJB

A;Residues: 66-93, 'XX', 96-115, 'XX', 118-134 <HAY>
A;Cross-references: GB:KD0662; NID:9164154; PID:g164158
C;Comment: This type of beta-C chain is found when anemia has been experimentally produced
C;Genetics:
A;Introns: 26/2; 100/3
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F;1-141/Domain: globin homology <GHB>
F;58/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match Similarity 100.0%; Score 10; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.00017; Length 141;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C;Species: Ovis orientalis musimon, Ovis ammon musimon (mouflon)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
C;Accession: A90232; A02396
R;Wilson, J.B.; Miller, A.; Huisman, T.H.J.
Biochem. Genet. 4, 677-688, 1970
A;Title: Production of hemoglobin C in the mouflon (*Ovis musimon pallas*, 1811) and the
peptides from the beta(B) and beta(C) chains.
A;Reference number: A90232; MUID:71089262
A;Accession: A90232
A;Molecule type: protein
A;Residues: 1-141 <WIL>
A;Note: compositions of tryptic peptides were determined; positions 100-111 were sequenced
C;Comment: This type of beta-C chain is found when anemia has been experimentally produced
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F;1-141/Domain: globin homology <GHB>
F;58/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match Similarity 100.0%; Score 10; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.00017; Length 141;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C;Species: Ovis orientalis musimon, Ovis ammon aries (domestic sheep)
C;Date: 30-Sep-1993 #sequence_revision 30-Jan-1998 #text_change 03-Mar-2000
C;Accession: S10074; B92027; A90045; A02396
R;Garner, K.J.; Linacre, J.B.
J. Mol. Evol. 28, 175-184, 1989
A;Title: A comparison of the beta(A)- and beta(B) globin gene clusters of sheep.
A;Reference number: S10073; MUID:89178744
A;Accession: S10074
A;Molecule type: DNA
A;Residues: 1-142 <GAR>
A;Cross-references: EMBL:X14728; NID:g1212; PIDN:CAA32B50.1; PID:g1213
A;Note: the authors translated the codon GTC for residue 30 as Ala
R;Boyer, S.H.; Hathaway, P.; Pascaio, F.; Bordley, J.; Orton, C.; Naughton, M.A.
J. Biol. Chem. 242, 2211-2223, 1967
A;Title: Differences in the amino acid sequences of tryptic peptides from three sheep
A;Reference number: A92027; MUID:67134347
A;Accession: B92027
A;Molecule type: protein
A;Residues: 2-64, 'B', 66-68, 'B', 70-71, 'Z', 73-74, 'BB', 77-82, 'Z', 84-85, 'Z', 87-94, 'B', 95,
A;Experimental source: Dorset breed
R;Wilson, J.B.; Edwards, W.C.; McDaniel, M.; Dobbs, M.M.; Huisman, T.H.J.
Arch. Biochem. Biophys. 115, 385-400, 1966
A;Title: The structure of sheep hemoglobins. II. The amino acid composition of the tr
A;Reference number: A90045
A;Accession: A90045
A;Molecule type: protein
A;Residues: 2-64, 'B', 66-68, 'B', 70-71, 'Z', 73-74, 'BB', 77-82, 'Z', 84-85, 'Z', 87-94, 'B', 96,
A;Experimental source: Rambouillet breed
A;Note: there are several discrepancies between the sequence in this paper and that g
C;Comment: This beta-C chain is produced when anemia is experimentally induced.
C;Genetics:
A;Introns: 26/2; 100/3
C;Complex: Two beta chains combine to form heterotetramers with two alpha chains to f
C;Function:
A;Description: in erythrocytes binds and transports molecular oxygen from lung to tis
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro
F;1-142/Domain: globin homology <GHB>
F;2-142/Product: hemoglobin beta-C chain #status experimental <MAT>
F;59/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;88/Binding site: heme iron (His) (proximal axial ligand) #status predicted

RESULT 7

HBSCR
hemoglobin beta-C chain - aoudad (tentative sequence)
C;Species: Ammotragus levia (aoudad, Barbary sheep)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
C;Accession: B90232; A02396
R;Wilson, J.B.; Miller, A.; Huisman, T.H.J.
Biochem. Genet. 4, 677-688, 1970
A;Title: Production of hemoglobin C in the moufflon (*Ovis musimon pallas*, 1811) and the
peptides from the beta(B) and beta(C) chains.
A;Reference number: A90232; MUID:71089262
A;Accession: B90232
A;Molecule type: protein
A;Residues: 1-141 <WIL>
A;Note: compositions of tryptic peptides were determined; positions 100-111 were sequenced
C;Comment: This type of beta-C chain is found when anemia has been experimentally produced
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F;1-141/Domain: globin homology <GHB>
F;58/Binding site: oxygen (His) (distal axial ligand) #status predicted

F;87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match Similarity 100.0%; Score 10; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.00017; Length 141;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C;Species: Ovis orientalis musimon, Ovis ammon aries (domestic sheep)
C;Date: 30-Sep-1993 #sequence_revision 30-Jan-1998 #text_change 03-Mar-2000
C;Accession: S10074; B92027; A90045; A02396
R;Garner, K.J.; Linacre, J.B.
J. Mol. Evol. 28, 175-184, 1989
A;Title: A comparison of the beta(A)- and beta(B) globin gene clusters of sheep.
A;Reference number: S10073; MUID:89178744
A;Accession: S10074
A;Molecule type: DNA
A;Residues: 1-142 <GAR>
A;Cross-references: EMBL:X14728; NID:g1212; PIDN:CAA32B50.1; PID:g1213
A;Note: the authors translated the codon GTC for residue 30 as Ala
R;Boyer, S.H.; Hathaway, P.; Pascaio, F.; Bordley, J.; Orton, C.; Naughton, M.A.
J. Biol. Chem. 242, 2211-2223, 1967
A;Title: Differences in the amino acid sequences of tryptic peptides from three sheep
A;Reference number: A92027; MUID:67134347
A;Accession: B92027
A;Molecule type: protein
A;Residues: 2-64, 'B', 66-68, 'B', 70-71, 'Z', 73-74, 'BB', 77-82, 'Z', 84-85, 'Z', 87-94, 'B', 96,
A;Experimental source: Dorset breed
R;Wilson, J.B.; Edwards, W.C.; McDaniel, M.; Dobbs, M.M.; Huisman, T.H.J.
Arch. Biochem. Biophys. 115, 385-400, 1966
A;Title: The structure of sheep hemoglobins. II. The amino acid composition of the tr
A;Reference number: A90045
A;Accession: A90045
A;Molecule type: protein
A;Residues: 2-64, 'B', 66-68, 'B', 70-71, 'Z', 73-74, 'BB', 77-82, 'Z', 84-85, 'Z', 87-94, 'B', 96,
A;Experimental source: Rambouillet breed
A;Note: there are several discrepancies between the sequence in this paper and that g
C;Comment: This beta-C chain is produced when anemia is experimentally induced.
C;Genetics:
A;Introns: 26/2; 100/3
C;Complex: Two beta chains combine to form heterotetramers with two alpha chains to f
C;Function:
A;Description: in erythrocytes binds and transports molecular oxygen from lung to tis
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro
F;1-142/Domain: globin homology <GHB>
F;2-142/Product: hemoglobin beta-C chain #status experimental <MAT>
F;59/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;88/Binding site: heme iron (His) (proximal axial ligand) #status predicted

RESULT 9

HBBOB
hemoglobin beta chain [validated] - bovine
N;Alternate names: hemoglobin-derived opioid peptide
N;Contains: LVV-hemorphin-7; WV-hemorphin-7

HBWA2

hemoglobin beta chain - yak

C;Species: Bos mutus grunniens (yak)

C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 03-Mar-2000

C;Accession: A02390

Ridibanthlunga, R.; Wiesner, H.; Brunitzer, G.

Biol. Chem. Hoppe-Seyler 366, 6368, 1985

A;Reference number: A90689; MUID:85225945

A;Contents: beta-I and beta-II alleles

A;Accession: A02390

A;Molecule type: protein

A;Residues: 1-145 <THE>

A;Note: the sequence from the beta-I allele differs from that shown in having 49-thr, 11

C;Comment: The beta-II allele is shown.

C;Note: The beta-II allele occurs much more frequently than the beta-I allele.

C;Superfamily: globin; globin homology

C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car

F;2-145;/domain: globin homology <GLB>

F;91/Binding site: oxygen (His) (distal axial ligand) #status Predicted

F;91/Binding site: heme iron (His) (proximal axial ligand) #status Predicted

Query Match

100.0%; Score 10; DB 1; Length 145;

Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10

Db 31 LVVYPWTQRF 40

A;Molecule type: protein

A;Residues: 1-145 <SHI>

C;Comment: This chain is one of five beta chain alleles.

C;Superfamily: globin; globin homology

C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car

F;2-145;/domain: globin homology <GLB>

F;91/Binding site: oxygen (His) (distal axial ligand) #status Predicted

F;91/Binding site: heme iron (His) (proximal axial ligand) #status Predicted

Query Match 100.0%; Score 10; DB 1; Length 145;

Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10

Db 31 LVVYPWTQRF 40

RESULT 16

RHSB

hemoglobin beta-B chain - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 24-Apr-1984 #sequence_revision 30-Jan-1998 #text_change 19-May-2000

C;Accession: S10073; A92027; I47082; A02394

R;Garner, K.J.; Lingrel, J.B.

J. Mol. Evol. 2, 175-184, 1989

A;Title: A comparison of the beta(A)- and beta(B)-globin gene clusters of sheep.

A;Reference number: S10073; MUID:89178744

A;Accession: S10073

A;Molecule type: DNA

A;Residues: 1-145 <GARL>

A;Cross-references: EMBL:X14727; NID:91208; PID:CA32849; 1; PID:91209

A;Note: the sequence of codons and residues 44-63 is repeated twice in the authors' t

R;Boyer, S.H.; Hattnaway, P.; Pascesio, F.; Bordley, J.; Orton, C.; Naughton, M.A.

J. Biol. Chem. 242, 2211-2232, 1967

A;Title: Differences in the amino acid sequences of tryptic peptides from three sheep

A;Reference number: A92027; MUID:67134347

A;Accession: A92027

A;Molecule type: Protein

A;Residues: 1-48, 3', 50-67, 3', 69-97, 3', 99, '2B', 102-145 <BOY>

R;Garner, K.J.; Lingrel, J.B.

Mol. Biol. Evol. 5, 134-140, 1988

RESULT 14

HBRN

hemoglobin beta chain - European moose

C;Species: Alces alces (European moose, elk)

C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 03-Mar-2000

C;Accession: A02392

R;Wiesner, H.; Brunitzer, G.

Hoppe-Seyler's Z. Physiol. Chem. 365, 1323-1330, 1984

A;Title: Zur intrinsischen Sauerstoffaffinitaet: die Primaerstruktur eines weiteren Rumi

A;Reference number: A91729; MUID:85078042

A;Accession: A02392

RESULT 18

A;Title: Structural organization of the beta-globin locus of beta-haplotype sheep.
A;Reference number: I47082; MUID:88216150
A;Accession: I47082
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-28 <GAR2>
A;Cross-references: GB:M19754; NID:9165890; PIDN:AAA31528.1; PID:9552420
A;Introns: 29/2; 103/3
C;Complex: two beta chains combine in heterotetramers with two alpha chains (see PIR:HAS)
C;Function: In erythrocytes binds and transports molecular oxygen from lung to tissue
A;Description: In erythrocytes binds and transports molecular oxygen from lung to tissue
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F1;145;Product: hemoglobin beta-B chain #status experimental <MAT>
F;2-145;Domain: globin homology <GLB>
F;62-145;Binding site: oxygen (His) (distal axial ligand) #status predicted
F;91;Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 31 LVVYPWTQRF 40

RESULT 17

HbSA
hemoglobin beta-A chain - sheep (tentative sequence)
C;Species: Ovis orientalis aries, Ovis ariam aries (domestic sheep)
C;Accession: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 31-Mar-2000
R;Beale, D.
Submitted to the Atlas, August 1967
A;Reference number: A94556
A;Accession: A94556
A;Molecule type: protein
A;Residues: 1-145 <BER1>
R;Beale, D.
Biochem. J. 103, 129-140, 1967
A;Title: A partial amino acid sequence for sheep haemoglobin A.
A;Reference number: A90237; MUID:67209244
A;Accession: A90237
A;Molecule type: protein
A;Residues: 1-145 <BER2>
R;Krebscher, P.J.; Coon, H.C.; Davis, A.; Harrison, M.; Nienhuis, A.W.
A;Title: Hemoglobin switching in sheep. Isolation of the fetal gamma-globin gene and den
s DNA.
A;Reference number: A92306; MUID:81117290
A;Accession: A92306
A;Molecule type: DNA
A;Residues: 1-28; 39-56, 'P', 58-59; 72-85; 104-145 <KR>
A;Cross-references: GB:k02820
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F;2-145;Domain: globin homology <GLB>
F;62;Binding site: oxygen (His) (distal axial ligand) #status predicted
F;91;Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 31 LVVYPWTQRF 40

RESULT 18

HBCTA
hemoglobin beta-A chain - goat
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 03-Mar-2000
C;Accession: A90017; I46170; I46273; I462028; A90047; A90049; A02395
R;Schon, E.A.; Cleary, M.L.; Hynes, J.R.; Lingrel, J.B.
Cell 27, 359-369, 1981
A;Title: Structure and evolution of goat gamma-, beta(c)- and beta(A)-globin genes: t
A;Reference number: A90817; MUID:82137075
A;Accession: A90817
A;Molecule type: DNA
A;Residues: 1-145 <SCB>
A;Cross-references: GB:M15387; NID:9164133; PIDN:AAA30913.1; PID:9164134
R;Cleary, M.L.; Haynes, J.R.; Schon, E.A.; Lingrel, J.B.
Nucleic Acids Res. 8, 4791-4802, 1980
A;Title: Identification by nucleotide sequence analysis of a goat pseudoglobin gene.
A;Reference number: I46169; MUID:81076616
A;Accession: I46170
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-29 <CLE1>
A;Cross-references: EMBL:V00152; NID:9961; PIDN:CAA23467.1; PID:9962
A;Accession: I46171
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 64-99 <CLB2>
A;Cross-references: EMBL:V00153; NID:9963; PIDN:CAA23468.1; PID:9669075
R;Haynes, J.R.; Rostock, P.R.; Schon, E.A.; Gallagher, P.M.; Burks, D.J.; Smith, K.;
J. Biol. Chem. 255, 6355-6367, 1980
A;Title: The isolation of the beta-a-, beta-c-, and gamma-globin genes and a presumpt
A;Reference number: I46273; MUID:80227766
A;Accession: I46273
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 64-97 <HAY1>
A;Cross-references: GB:K00657; NID:9164128; PIDN:AAA30911.1; PID:9552351
A;Accession: I46274
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 114-119 <HAY2>
A;Cross-references: GB:K00658; NID:9164129; PIDN:AAA30912.1; PID:9552352
R;Huisman, T.H.J.; Adams, H.R.; Dimmock, M.O.; Edwards, W.E.; Wilson, J.B.
J. Biol. Chem. 242, 2534-2541, 1967
A;Title: The structure of goat hemoglobins. I. Structural studies of the beta chains
A;Reference number: A92028; MUID:67165362
A;Accession: A92028
A;Molecule type: protein
A;Residues: 1-145 <HUI>
A;Experimental source: A allele, partial sequence
R;Adams, H.R.; Boyd, E.M.; Wilson, J.B.; Miller, A.; Huisman, T.H.J.
Arch. Biochem. Biophys. 127, 398-405, 1968
A;Title: The structure of goat hemoglobins. III. Hemoglobin D, a beta chain variant w
A;Reference number: A90047; MUID:69036192
A;Accession: A90047
A;Molecule type: protein
A;Residues: 1-19, H, 21-145 <ADA>
A;Experimental source: D allele, partial sequence
R;Wrightson, R.N.; Wilson, J.B.; Miller, A.; Huisman, T.H.J.
Arch. Biochem. Biophys. 138, 451-56, 1970
A;Title: The structure of goat hemoglobins. IV. A third beta chain variant (beta-E) w
A;Reference number: A90049; MUID:70252721
A;Accession: A90049
A;Molecule type: protein
A;Residues: 1-85, 'H', 87-102, 'R', 104-123, 'V', 125-145 <WRI>
A;Experimental source: E allele, partial sequence
A;Comment: The A allele sequence is shown.
C;Genetics:
A;Introns: 29/2; 103/3
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
F;62;Binding site: oxygen (His) (distal axial ligand) #status predicted

F;91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100 0%; Score 10; DB 1; Length 145;
 Best Local Similarity 100 0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 31 LVVYPWTQRF 40

RESULT 19

HBBOF
 hemoglobin beta chain, fetal - bovine
 N; Alternate names: hemoglobin gamma chain
 C; Species: Bos primigenius taurinus (cattle)
 C; Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Mar-2000
 C; Accession: A93504; A90549; A02398
 R; Schimenti, J.C.; Duncan, C.H.
 Nucleic Acids Res. 12, 1641-1655, 1984
 A; Title: Ruminant globin gene structures suggest an evolutionary role for Alu-type repeats
 A; Reference number: A93504; MUID:84144058

A; Molecule type: DNA
 A; Residues: 1-145 <SCH>
 A; Cross-references: GB:X00354; NID:9392; PIDN:CAA25101.1; PID:9393
 R; Babin, D.R.; Schroeder, W.A.; Shelton, J.R.; Shelton, J.B.; Robberson, B.
 Biochemistry 5, 1291-1310, 1996
 A; Title: The amino acid sequence of the gamma chain of bovine fetal hemoglobin.
 A; Reference number: A90549; MUID:67089183

A; Accession: A90549
 A; Molecule type: protein
 A; Residues: 1-145 <BBB>
 C; Genetics:
 A; Introns: 29/2; 103/3
 C; Superfamily: globin; globin homology
 C; Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F; 2-145/Domain: globin homology <GLB>
 F; 62/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F; 91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100 0%; Score 10; DB 1; Length 145;
 Best Local Similarity 100 0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 31 LVVYPWTQRF 40

RESULT 20

HGTF
 hemoglobin beta chain, fetal - goat
 N; Alternate names: hemoglobin gamma chain [mismosomer]
 C; Species: Capra aegagrus hircus (domestic goat)
 C; Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 03-Mar-2000
 C; Accession: A03399; A91710; I46279; I46280
 R; Schon, E.A.; Cleary, M.L.; Haynes, J.R.; Lingrel, J.E.
 Cell 27, 359-369, 1981
 A; Title: Structure and evolution of goat gamma-, beta(c)- and beta(A)-globin genes: three
 A; Reference number: A90817; MUID:82137075
 A; Accession: A03399
 A; Molecule type: SCHE
 A; Residues: 1-145 <SCH>
 A; Cross-references: GB:ML5388; NID:9164169; PIDN:AAA30951.1; PID:9164170
 R; Kleinschmidt, T.; Braumüller, G.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 789-796, 1982
 A; Title: Die Primaestruktur der gamma-Ketten der foetalen Haemoglobine von Schaf (Ovis
 A; Reference number: A91710; MUID:83005406
 A; Accession: A91710
 A; Molecule type: protein

A; Residues: 1-145 <KLE>
 R; Hayes, J.R.; Rosteck, P.R.; Schon, E.A.; Gallagher, P.M.; Burks, D.J.; Smith, K.;
 J. Biol. Chem. 255, 6355-6367, 1980
 A; Title: The isolation of the beta-a-, beta-c-, and gamma-globin genes and a presumptive
 A; Reference number: 146273; MUID:80227766
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 52-97 <HAY1>
 A; Cross-references: GB:K00663; NID:9164164; PIDN:AAA30923.1; PID:9164167
 A; Accession: I46280
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 104-118, 'XXX' 122-123, 'G' 125-139 <HAY2>
 A; Cross-references: GB:k00664; NID:9164165; PIDN:AAA30924.1; PID:9552354
 C; Comment: This is regarded as a beta chain produced by the fetus, not as a gamma chain
 C; Superfamily: globin; globin homology
 C; Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F; 1-145/Product: hemoglobin beta chain, fetal #status experimental <MAT>
 F; 2-145/Domain: globin homology <GLB>
 F; 62/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F; 91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100 0%; Score 10; DB 1; Length 145;
 Best Local Similarity 100 0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 31 LVVYPWTQRF 40

RESULT 21

HGS
 hemoglobin beta chain, fetal - sheep
 N; Alternate names: hemoglobin gamma chain [mismosomer]
 C; Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Mar-2000
 C; Accession: B92306; S45297; A90610; A92306
 R; Kretschmer, P.J.; Coon, H.C.; Davis, A.; Harrison, M.; Nienhuis, A.W.
 J. Biol. Chem. 256, 1975-1982, 1981
 A; Title: Hemoglobin switching in sheep. Isolation of the fetal gamma-globin gene and
 s DNA.
 A; Reference number: A92306; MUID:81117290
 A; Accession: B92306
 A; Molecule type: DNA
 A; Residues: 1-29-52-95-104-145 <KRE>
 A; Cross-references: GB:K02824; NID:9165901; PIDN:AAA31533.1; PID:9552423; GB:K02825;
 R; Saban, J.; King, D.
 Blochim. Biophys. Acta 1218, 87-90, 1994
 A; Title: Sequence of the sheep fetal beta globin gene and flanking region.
 A; Reference number: S45297; MUID:94250699
 A; Accession: S45297
 A; Molecule type: DNA
 A; Residues: 1-17, 30-47, 'F' 49-145 <SAB>
 A; Cross-references: EMBL:U01378; NID:9437113; PIDN:AAA19218.1; PID:9437114
 R; Darbre, P.D.; Lehmann, H.
 Blochim. Biophys. Acta 446, 10-18, 1976
 A; Title: The gamma chain of the lamb
 A; Reference number: A90610; MUID:7702158
 A; Accession: A90610
 A; Molecule type: protein
 A; Residues: 1-118, EG, I21-145 <DAR>
 C; Comment: This is regarded as a beta chain produced by the fetus, not as a gamma chain
 C; Complex: Two gamma chains combine in heterotetramers with two alpha chains to form
 C; Function: In erythrocytes binds and transports molecular oxygen from placenta to
 C; Superfamily: globin; globin homology
 C; Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F; 1-145/Product: hemoglobin beta chain, fetal #status experimental <MAT>

F;2-145/Domain: globin homology <GLB>
F;91/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match	Score	DB	Length	Indels	Gaps	Mismatches	Conservative	Best Local Similarity	Pred.	No.	0.00017;
Qy 1 LVVYPWTQRF 10	100.0%	1	145	0	0	0	0	100.0%	0	0	
Db 31 LVVYPWTQRF 40											

RESULT 22

B58794 hemoglobin beta chain - domestic water buffalo

C;Species: *Bubalus arnee bubalis* (domestic water buffalo)

C;Date: 07-Aug-1998 #sequence_revision 07-Aug-1998 #text_change 20-Jun-2000

C;Accession: P58794; R49141

R;Ferranti, P.; Malorni, A.; Marino, G.; Pucci, P.; Di Luccia, A.; Ferrara, L.

Int. J. Mass Spectrom. Ion Process. 111, 287-300, 1991

A;Title: FAB overlapping: a strategy for sequencing homologous proteins.

A;Reference number: A58794

A;Accession: B58794

A;Molecule type: protein

A;Residues: 1-145 <FER>

A;Title: River buffalo (*Bubalus bubalis* L.) AA phenotype haemoglobins: characterization of the primary structure of the constitutive chains by mass spectrometry.

A;Reference number: A49141; MUID:92362189

A;Accession: A49141

A;Molecule type: protein

A;Residues: 1-145 <FE2>

A;Experimental source: AA phenotype

A;Note: sequence extracted from NCBI backbone (NCBIP:111135)

C;Superfamily: globin; globin homology

C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F;2-145/Domain: globin homology <GLB>

F;91/Binding site: oxygen (His) (distal axial ligand) #status predicted

F;91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 2; Length 145; Pred. No. 0.00017; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10

Db 31 LVVYPWTQRF 40

RESULT 24

C25727 hemoglobin beta chain - European bison

C;Species: *Bison bonasus* (European bison)

C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 19-May-2000

C;Accession: C25727

R;Hazur, G.; Muller, E.; Braunitzer, G.; Wiesner, H.

Biol. Chem. Hoppe-Seyler 367, 417-423, 1986

A;Title: Intrinsische Sauerstoffaffinitat der Hämoglobine: das Hämoglobin des Wisents

A;Reference number: A90706; MUID:86296178

A;Accession: C25727

A;Molecule type: protein

A;Residues: 1-145 <MAZ>

C;Superfamily: globin; globin homology

C;Keywords: blood; chromoprotein; heme; iron; metalloprotein; oxygen carrier

F;2-145/Domain: globin homology <GLB>

F;91/Binding site: oxygen (His) (distal axial ligand) #status predicted

F;91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 2; Length 145; Pred. No. 0.00017; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10

Db 31 LVVYPWTQRF 40

RESULT 25

HB2P hemoglobin beta chain - pygmy chimpanzee

C;Species: *Pan paniscus* (pygmy chimpanzee, bonobo)

C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 03-Mar-2000

C;Accession: D93303

R;Goodman, M.; Braunquier, G.; Stangl, A.; Schrank, B.

Nature 303, 546-548, 1983

A;Title: Evidence on human origins from haemoglobins of African apes.

A;Reference number: A93303; MUID:83219265

A;Accession: D93303

A;Molecule type: protein

A;Residues: 1-146 <GOO>

C;Superfamily: globin; globin homology

C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F;3-146/Domain: globin homology <GLB>

F;1,2,82,143/Binding site: 2,3-diphosphoglycerate (Val, His, Lys, His) #status predicted

F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146; Pred. No. 0.00017; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10

Db 32 LVVYPWTQRF 41

RESULT 26

HBTG1 hemoglobin beta chain - common gibbon (tentative sequence)

C;Species: Hylobates lar (common gibbon, white-handed gibbon)
 C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 03-Mar-2000
 C;Accession: A02353
 R;Buyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.;
 Biochem. Genet. 5, 405-448, 1971
 A;Reference number: A90333; MUID:72020149
 A;Accession: A02353
 A;Molecule type: protein
 A;Residues: 1-146 <R01>
 C;Comment: A common allelic sequence has 80-Asp and 87-Lys, and an uncommon allelic seq.
 C;Superfamily: globin; globin homology
 F;3-146/domain: globin homology <GLB>
 F;63/Hist: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 27

HBMQP
 hemoglobin beta chain - hanuman langur
 C;Species: Presbytis entellus (hanuman langur)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 C;Accession: A02354
 R;Matsuda, G.; Maita, T.; Nakashima, Y.; Barnabas, J.; Ranjekar, P.K.; Gandhi, N.S.
 Int. J. Pept. Protein Res. 5, 423-425, 1973
 A;Title: The primary structures of the alpha and beta poly-peptide chains of adult hemog.
 A;Reference number: A02250; MUID:74115166
 A;Accession: B02250
 A;Molecule type: protein
 A;Residues: 1-146 <WAK>
 C;Superfamily: globin; globin homology
 F;3-146/domain: globin homology <GLB>
 F;92/Binding site: oxygen (His) (distal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 29

HBMQPM
 hemoglobin beta chain - pig-tailed macaque
 C;Species: Macaca nemestrina (pig-tailed macaque)
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 03-Mar-2000
 C;Accession: S10689
 R;Nute, P.B.; Patarras, H.A.
 Am. J. Phys. Anthropol. 40, 75-82, 1974
 A;Title: Amino acid compositions of the tryptic peptides comprising the beta-hemog.
 A;Reference number: S10689; MUID:74126665
 A;Accession: S10689
 A;Molecule type: protein
 A;Residues: 1-146 <NOT>
 C;Superfamily: globin; globin homology
 F;3-146/domain: globin homology <GLB>
 F;92/Binding site: oxygen (His) (distal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 30

HBMQC
 hemoglobin beta chain - crab-eating macaque
 C;Species: Macaca fascicularis (crab-eating macaque)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 C;Accession: A29665; A04623; A02354
 R;Savatier, P.; Traubachet, G.; Chebloune, Y.; Faure, C.; Verdier, G.; Nigro, V.M.
 J. Mol. Evol. 24, 309-318, 1987
 A;Title: Nucleotide sequence of the beta-globin genes in gorilla and macaque: the ori.
 A;Reference number: A29665; MUID:87254238
 A;Accession: A29665
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-120 <SAV>
 A;Cross-references: EMBL:X05665; NID:930042; PID:NC_002153.1; PID:91333691
 A;Experimental source: species designated as Macaca cynomolgus
 A;Note: Initiator Met not translated
 R;Wade, P.T.; Barnicot, N.A.; Huehns, E.R.
 Biochim. Biophys. Acta 221, 450-465, 1970
 A;Title: Structural studies on the major and minor haemoglobin of the monkey Macaca-i
 A;Reference number: A04623; MUID:71108403
 A;Accession: A04623
 A;Molecule type: protein
 A;Residues: 1-146 <WAD>
 A;Genetics:
 A;Introns: 30/3; 10/4/3
 C;Superfamily: globin; globin homology
 F;3-146/domain: globin homology <GLB>
 F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

RESULT 28

HBMQJ
 hemoglobin beta chain - Japanese macaque
 C;Species: Macaca fuscata (Japanese macaque)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 C;Accession: A04622; A02354
 R;Matsuda, G.; Maita, T.; Ota, H.; Tachikawa, I.; Tanaka, Y.; Araya, A.; Nakashima, Y.
 Int. J. Protein Res. 3, 53-55, 1971
 A;Title: The primary structure of the beta polypeptide chain of adult hemoglobin of the
 A;Reference number: A04622; MUID:7203053
 A;Accession: A04622
 A;Molecule type: protein
 A;Residues: 1-146 <WAT>
 C;Superfamily: globin; globin homology
 F;3-146/domain: globin homology <GLB>
 F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; C; Accession: A04620; A02354
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 C; Species: *Cercopithecus aethiops* (green monkey, grivet)
 C; Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 C; Accession: B02252; A02354
 R; Matsuda, G.; Maita, T.; Watanabe, B.; Araya, A.; Morokuma, K.; Goodman, M.; Prychadko,
 Hoppe-Seyler's Z. Physiol. Chem. 354, 1153-1155, 1973
 A; Title: The amino acid sequences of the alpha and beta polypeptide chains of adult heme
 A; Reference number: A02252; MUID:75040050
 A; Accession: B02252
 A; Molecule type: protein
 A; Residues: 1-146 <NTR>
 C; Superfamily: globin; globin homology
 C; Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
 F; 3-146/Domain: globin homology <GLB>
 F; 63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 R; 92/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; C; Accession: A04620; A02354
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 C; Species: *Papio sphinx*, *Mandrillus sphinx* (mandrill)
 C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 03-Mar-2000
 C; Accession: S00540
 R; Lin, H.X.; Kleinschmidt, T.; Braunitzer, G.; Goeltzenboth, R.
 Biol. Chem. Hoppe-Seyler 369, 209-216, 1988
 A; Title: The primary structure of the mandrill (*Mandrillus sphinx*, Primates) hemoglobin.
 A; Reference number: S00526; MUID:88293710
 A; Accession: S00540
 A; Molecule type: protein
 A; Residues: 1-146 <LIN>
 C; Superfamily: globin; globin homology
 C; Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F; 3-146/Domain: globin homology <GLB>
 F; 63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 R; 92/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; C; Accession: A04620; A02354
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 C; Species: *Cercopithecus aethiops* (green monkey, grivet)
 C; Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 C; Accession: A04620; A02354
 R; Nutt, P.E.; Manoney, W.C.
 Hemoglobin 4, 109-123, 1980
 A; Title: Complete primary structure of the beta chain from the hemoglobin of a baboon
 A; Reference number: A04624; MUID:80227364
 A; Accession: A04624
 A; Molecule type: protein
 A; Residues: 1-146 <NUR>
 C; Superfamily: globin; globin homology
 C; Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
 F; 3-146/Domain: globin homology <GLB>
 F; 63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 R; 92/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; C; Accession: A04620; A02354
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 C; Species: *Cercopithecus torquatus* (red-crowned mangabey, white-collared mangabey)
 C; Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 C; Accession: A04621; A02354
 R; Cook, C.N.; Barnicot, N.A.
 unpublished results, cited in Hewett-Emmett, D., Ph.D. thesis, University of London,
 Fasman, G.D., ed., PP 441-460, Chemical Rubber Co., Cleveland, 1976
 A; Accession: A04621
 A; Molecule type: protein
 A; Residues: 1-146 <COO>
 C; Superfamily: globin; globin homology
 C; Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
 F; 3-146/Domain: globin homology <GLB>
 F; 63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 R; 92/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 RESULT 33
 HBAG
 hemoglobin beta chain - gelada baboon
 C; Species: *Theopithecus gelada* (gelada baboon)
 C; Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 " "

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTORF 10
 Db 32 LVVYPWTORF 41

RESULT 36

HBMOB
 hemoglobin beta chain - red colobus
 C;Species: Colobus badius (red colobus)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 C;Accession: A04620; A02354
 R;Hewett-Emmett, D.; Barnicot, N.A.
 unpublished results, cited in Hewett-Emmett, D., Ph.D. thesis, University of London, 1976
 Rasmussen, G.D., ed., pp.41-460, Chemical Rubber Co., Cleveland, 1976
 A;Reference number: A04620
 A;Accession: B04620
 A;Molecule type: protein
 A;Residues: 1-146 <HBW>
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F;3-146/Domain: globin homology <GLB>
 F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTORF 10
 Db 32 LVVYPWTORF 41

RESULT 37

HBMOB
 hemoglobin beta chain - brown-headed tamarin (tentative sequence)
 C;Species: Saguinus fuscicollis (brown-headed tamarin)
 C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 03-Mar-2000
 C;Accession: A02359
 R;Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.
 Biochem. Genet. 5, 405-448, 1971
 A;Title: Primate hemoglobins: some sequences and some proposals concerning the characterization of the hemoglobins
 A;Reference number: A90233; MUID:72020149
 A;Accession: A02359
 A;Molecule type: protein
 A;Residues: 1-146 <BOY>
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F;3-146/Domain: globin homology <GLB>
 F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTORF 10
 Db 32 LVVYPWTORF 41

RESULT 39

HBMM
 hemoglobin beta chain - moustached tamarin (tentative sequence)
 C;Species: Saguinus mystax (moustached tamarin)
 C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 03-Mar-2000
 C;Accession: A02359
 R;Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.
 Biochem. Genet. 5, 405-448, 1971
 A;Title: Primate hemoglobins: some sequences and some proposals concerning the characterization of the hemoglobins
 A;Reference number: A90233; MUID:72020149
 A;Accession: A02359
 A;Molecule type: protein
 A;Residues: 1-146 <BOY>
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F;3-146/Domain: globin homology <GLB>
 F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTORF 10
 Db 32 LVVYPWTORF 41

RESULT 40

HCCB
 hemoglobin beta chain - black-tailed marmoset
 C;Species: Callithrix argentata (black-tailed marmoset)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 C;Accession: S06513
 R;Maita, T.; Hayashida, M.; Matsuda, G.
 J. Biochem. 95, 805-813, 1984
 A;Title: primary structures of adult hemoglobins of silvery marmoset, Callithrix argentea
 A;Reference number: S06512; MUID:84212383
 A;Accession: S06513
 A;Molecule type: protein
 A;Residues: 1-146 <MAI>
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F;3-146/Domain: globin homology <GLB>
 F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVPPWTQRF 10
Db 32 LVVPPWTQRF 41

RESULT 41

HBKMAA hemoglobin beta chain - white-fronted capuchin hemoglobin (white-fronted capuchin, Pale-fronted capuchin)
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 11-May-2000
C;Accession: A02361
R;Nite, P.E.; Sullivan, B.
Comp. Biochem. Physiol. B, 39, 797-814, 1971
A;Title: Primate hemoglobins: their structure, function and evolution. I. Amino acid con
A;Reference number: A02361; MUID:72076589
A;Accession: A02361
A;Molecule type: protein
A;Residues: 1-146 <NUT>
A;Note: 13-The was found in half of the beta chains from one monkey
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
F;3-146/Domain: globin homology <GLB>
F;92/Binding site: oxygen (His) (distal axial ligand) #status predicted
Query Match 100.0%; Score 10; DB 1; Length 146;
Best local similarity 100.0%; Pred. No. 0.00017; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LVVPPWTQRF 10
Db 32 LVVPPWTQRF 41

RESULT 42

HBKMAA hemoglobin beta chain - brown capuchin hemoglobin (brown capuchin, black-capped capuchin)
C;Species: Cebus apella (brown capuchin, black-capped capuchin)
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 03-Mar-2000
C;Accession: A02362
R;Matanabe, B.
Seikagaku 46, 255-267, 1974
A;Title: Amino acid sequences of the tryptic peptides from the beta chain of hemoglobin
A;Reference number: A02362; MUID:75042140
A;Accession: A02362
A;Molecule type: protein
A;Residues: 1-146 <WAT>
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
F;3-146/Domain: globin homology <GLB>
F;92/Binding site: oxygen (His) (distal axial ligand) #status predicted
Query Match 100.0%; Score 10; DB 1; Length 146;
Best local similarity 100.0%; Pred. No. 0.00017; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LVVPPWTQRF 10
Db 32 LVVPPWTQRF 41

RESULT 43

HBKMH hemoglobin beta chain - long-haired spider monkey hemoglobin beta chain - long-haired spider monkey
C;Species: Atelopus belzebul (long-haired spider monkey)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 03-Mar-2000
C;Accession: B90233; A02355
R;Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.
Biochem. Genet. 5, 405-448, 1971
A;Title: Primate hemoglobins: some sequences and some proposals concerning the charac
A;Reference number: A90233; MUID:72020149
A;Accession: B90233
A;Molecule type: protein
A;Residues: 1-146 <BOY>
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
F;3-146/Domain: globin homology <GLB>
F;92/Binding site: oxygen (His) (distal axial ligand) #status predicted
Query Match 100.0%; Score 10; DB 1; Length 146;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LVVPPWTQRF 10
Db 32 LVVPPWTQRF 41

RESULT 43

HBKMN hemoglobin beta chain - douroucouli (tentative sequence)
C;Species: Atelus trivirgatus (douroucouli, night monkey, owl monkey)
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 03-Mar-2000
C;Accession: A02356

Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 :>

RESULT 46

HBMKK
 hemoglobin beta chain - black spider monkey
 C;Species: Atelopus paniscus (black spider monkey)
 C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 03-Mar-2000
 C;Accession: A0034; A0355
 R;Boyer, S.H.; Crosby, E.F.; Fuller, G.F.; Noyes, A.N.; Adams, J.G.
 Ann. N. Y. Acad. Sci. 165, 360-377, 1969
 A;Title: The structure and biosynthesis of hemoglobins A and A-2 in the new world primate
 A;Reference number: A9034; MUID:7031568
 A;Accession: A9034
 A;Molecule type: protein
 A;Residues: 1-146 <BOY>
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; metalloprotein
 F;3-146/Domain: globin homology <GLB>
 F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 47

HBMS
 hemoglobin beta chain - common squirrel monkey (tentative sequence)
 C;Species: Samirri sciurus (common squirrel monkey)
 C;Accession: A02357
 C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 03-Mar-2000
 R;Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.; V
 A;Title: Primate hemoglobins: some sequences and some proposals concerning the character
 A;Reference number: A90233; MUID:72020149
 A;Accession: A02357
 A;Molecule type: protein
 A;Residues: 1-146 <BOY>
 A;Note: an allelic sequence has 76-thr
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F;3-146/Domain: globin homology <GLB>
 F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 49

HBHU
 hemoglobin delta chain - human
 C;Species: Homo sapiens (man)
 C;Date: 30-Apr-1980 #sequence_revision 30-Apr-1980 #text_change 03-Mar-2000
 R;Spritz, R.A.; Deriel, J.K.; Forget, B.G.; Weissman, S.M.
 Cell 21, 639-646, 1980
 A;Title: Complete nucleotide sequence of the human delta-globin gene.
 A;Reference number: A90804; MUID:81064666
 A;Accession: A90804
 A;Molecule type: DNA
 A;Residues: 1-146 <SPR>
 A;Cross-references: GB:v00505; NID:q30510; PIDN:CAA23763.1; PID:q30511
 R;Braunitzer, G.; Schrank, B.; Staagl, A.; Grillemeier, M.
 Hoppe-Seyler's Z. Physiol. Chem. 359, 777-783, 1978
 A;Title: Notiz zur Sequenz der delta Ketten der menschlichen Haemoglobine (Hb A-2 = a
 A;Reference number: A91678; MUID:78240319
 A;Accession: A91678
 A;Molecule type: protein
 A;Residues: 1-146 <BRA>
 C;Genetics:
 A;Gene: GDI; HBD
 A;Cross-references: GDB:119298; OMIM:142000
 A;Map position: 11p15.5-11p15.5
 C;Complex: two delta chains combine in heterotetramers with two alpha chains (see PIR
 A;Function:
 A;Description: in erythrocytes binds and transports molecular oxygen from lung to tis
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro
 F;3-146/Domain: globin homology <GLB>
 F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 48

HBEMA
 hemoglobin beta chain - Amazon manatee
 C;Species: Trichechus inunguis (Amazon manatee, Brazilian manatee)
 C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 03-Mar-2000
 C;Accession: S00821; B24929

RESULT 50
 HbCZ
 hemoglobin delta chain - chimpanzee (tentative sequence)
 C;Species: Pan troglodytes (chimpanzee)
 C;Accession: C90233; A93402; A02364
 R;Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.; V
 Biochem. Genet. 5, 405-448, 1971
 A;Title: Primate hemoglobins: some sequences and some proposals concerning the character
 A;Reference number: A90233; MUID:72020149
 A;Accession: C90233
 A;Molecule type: protein
 A;Residues: 1-146 <BOY>
 R;de Jong, W.W.W.
 Nature New Biol. 234, 176-177, 1971
 A;Title: Structure of the delta-chain of chimpanzee haemoglobin A-2.
 A;Reference number: A03402; MUID:72020100
 A;Accession: A93402
 A;Molecule type: protein
 A;Residues: 1-146 <DEJ>
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
 F;3-146/Domain: globin homology <GLB>
 F;3-146/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 R;de Jong, W.W.W.
 Nature New Biol. 234, 176-177, 1971
 A;Title: Structure of the delta-chain of chimpanzee haemoglobin A-2.
 A;Reference number: A03402; MUID:72020100
 A;Accession: A93402
 A;Molecule type: protein
 A;Residues: 1-146 <DEJ>
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
 F;3-146/Domain: globin homology <GLB>
 F;3-146/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVVPWTORF 10
 |||||||
 Db 32 LVVVPWTORF 41

RESULT 51
 HDGQ
 hemoglobin delta chain - gorilla (tentative sequence)
 C;Species: Gorilla gorilla (gorilla)
 C;Accession: D90233; A02364
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
 C;Accession: D90233; A02364
 R;Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.; V
 Biochem. Genet. 5, 405-448, 1971
 A;Title: Primate hemoglobins: some sequences and some proposals concerning the character
 A;Reference number: A90233; MUID:72020149
 A;Accession: D90233
 A;Molecule type: protein
 A;Residues: 1-146 <BOY>
 A;Note: an allele of the gorilla sequence has 126-Ala
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
 F;3-146/Domain: globin homology <GLB>
 F;3-146/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVVPWTORF 10
 |||||||
 Db 32 LVVVPWTORF 41

RESULT 52
 HDGK
 hemoglobin delta chain - gibbon (tentative sequence)
 C;Species: Hylobates sp. (gibbon)
 C;Accession: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
 C;Accession: E90233; A02364
 R;Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVVPWTORF 10
 |||||||
 Db 32 LVVVPWTORF 41

RESULT 53
 HDMKH
 hemoglobin delta chain - black-handed spider monkey
 C;Species: Atelopus geoffroyi (black-handed spider monkey)
 C;Accession: A31523; B02365
 R;Spritz, R.A.; Glebel, L.B.
 Mol. Biol. Evol. 5, 21-29, 1988
 A;Title: The structure and evolution of the spider monkey delta-globin gene.
 A;Reference number: A31523; MUID:88189005
 A;Accession: A31523
 A;Molecule type: DNA
 A;Residues: 1-146 <SPR>
 A;Cross-References: GB:M19061; NID:9342379; PIDN:AB00793.1; PID:9342380
 A;Note: the authors translated the codon AGG for residue 132 as Glu
 R;Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.
 Biochem. Genet. 5, 405-448, 1971
 A;Title: Primate hemoglobins: some sequences and some proposals concerning the character
 A;Reference number: A90233; MUID:72020149
 A;Accession: B02365
 A;Molecule type: protein
 A;Residues: 1-4, 'G', 6-8, 'S', 10-46, 'A', 48-51, 'D', 53-146 <BOY>
 A;Note: three alleles of the sequence shown have 6-Lys, 9-Ala, and 69-Asp, respective
 C;Genetics:
 A;Introns: 30/2; 104/3
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
 F;3-146/Domain: globin homology <GLB>
 F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVVPWTORF 10
 |||||||
 Db 32 LVVVPWTORF 41

A;Title: Primate hemoglobins: some sequences and some proposals concerning the character
A;Reference number: A90233; MUID:72020149
A;Accession: CO2365
A;Molecule type: protein
A;Residues: 1-146 <BOY>
A;Note: three alleles of the sequence shown have 6-Lys, 9-Ala, and 69-Asp, respectively
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F;3-146/Domain: globin homology <GLB>
F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWQRF 10
Db 32 LVVYPWQRF 41

RESULT 55
HDMKTM
hemoglobin delta chain - moustached tamarin (tentative sequence)
C;Species: *Saguinus mystax* (moustached tamarin)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
C;Accession: D02365; A02365
R;Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.; Blochim. Genet. 5, 405-448, 1971
A;Title: Primate hemoglobins: some sequences and some proposals concerning the character
A;Reference number: A90233; MUID:72020149
A;Accession: D02365
A;Molecule type: protein
A;Residues: 1-146 <BOY>
A;Note: residues 16 and 12 may be Gly and Ser, respectively
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F;3-146/Domain: globin homology <GLB>
F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWQRF 10
Db 32 LVVYPWQRF 41

RESULT 57
HMKDU
hemoglobin delta chain - doucocolli (tentative sequence)
C;Species: *Autus trivirgatus* (doucocolli, night monkey, owl monkey)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
C;Accession: F02365; A02365
R;Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.; Blochim. Genet. 5, 405-448, 1971
A;Title: Primate hemoglobins: some sequences and some proposals concerning the character
A;Reference number: A90233; MUID:72020149
A;Accession: F02365
A;Molecule type: protein
A;Residues: 1-146 <BOY>
A;Note: residue 125 may be Gln and residue 127 or 131 may be Leu
A;Note: an allelic sequence has 120-Asn
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F;3-146/Domain: globin homology <GLB>
F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWQRF 10
Db 32 LVVYPWQRF 41

RESULT 58
HMKSQ
hemoglobin delta chain - common squirrel monkey (tentative sequence)
C;Species: *Saimiri scureus* (common squirrel monkey)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
C;Accession: G02365; A02365
R;Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.; Blochim. Genet. 5, 405-448, 1971
A;Title: Primate hemoglobins: some sequences and some proposals concerning the character
A;Reference number: A90233; MUID:72020149
A;Accession: G02365
A;Molecule type: protein
A;Residues: 1-146 <BOY>
A;Note: residues 16 and 12 may be Gly and Ser, respectively. Residues 51 and 58 may be
A;Note: an allelic sequence has 121-Gln
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F;3-146/Domain: globin homology <GLB>
F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWQRF 10
Db 32 LVVYPWQRF 41

RESULT 59
HBLSR
hemoglobin delta chain - black-and-red tamarin (tentative sequence)
C;Species: *Saguinus nigricollis* (black-and-red tamarin)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
C;Accession: E02365; A02365
R;Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.; Blochim. Genet. 5, 405-448, 1971
A;Title: Primate hemoglobins: some sequences and some proposals concerning the character
A;Reference number: A90233; MUID:72020149
A;Accession: E02365
A;Molecule type: protein
A;Residues: 1-146 <BOY>
A;Note: residues 16 and 12 may be Gly and Ser, respectively
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F;3-146/Domain: globin homology <GLB>
F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 hemoglobin beta chain - slow loris
 C;Species: Nycticebus coucang (slow loris)
 C;Date: 24-Apr-1984 #sequence_revision 31-Dec-1991 #text_change 03-Mar-2000
 C;Accession: A02365
 R;Matsuda, G.; Maita, T.; Watanabe, B.; Ota, H.; Araya, A.; Goodman, M.; Prychodko, W.
 A;Title: The primary structures of the alpha and beta polypeptide chains of adult hemoglo
 A;Reference number: A91167; MUID:4115165
 A;Accession: A02366
 A;Molecule type: protein
 A;Residues: 1-146 <WAT>
 C;Superfamily: globin; globin homology
 F;3-146/domain: globin; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F;3-146/domain: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVVPWTQRF 10
 Db 32 LVVVPWTQRF 41

RESULT 60

HBLRN
 hemoglobin beta chain - slender loris
 C;Species: Loris tardigradus (slender loris)
 C;Accession: B01949
 R;Maita, T.; Goodman, M.; Matsuda, G.
 J; Blochem, 84, 377-383, 1978
 A;Title: Amino acid sequences of the alpha and beta chains of adult hemoglobin of the slender loris
 A;Reference number: A91169; MUID:79027141
 A;Accession: B01949
 A;Molecule type: protein
 A;Residues: 1-146 <WAT>
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F;3-146/domain: globin homology <GLB>
 F;92/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVVPWTQRF 10
 Db 32 LVVVPWTQRF 41

RESULT 61

HBCC
 hemoglobin beta-I chain - thick-tailed bush baby
 C;Species: Galago crassicaudatus, Otolemur crassicaudatus (thick-tailed bush baby)
 C;Accession: A02367
 R;Watanabe, B.; Fujii, T.; Nakashima, Y.; Maita, T.; Matsuda, G.
 A;Title: Amino-acid sequences of the alpha and beta chains of adult hemoglobins of the thick-tailed bush baby
 A;Reference number: A90083; MUID:85225956
 A;Accession: A02367
 A;Molecule type: protein
 A;Residues: 1-146 <WAT>
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F;3-146/domain: globin homology <GLB>
 F;92/Binding site: oxygen (His) (distal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVVPWTQRF 10
 Db 32 LVVVPWTQRF 41

RESULT 64

HBLEF
 hemoglobin beta chain - brown lemur (tentative sequence)

C;Species: Lemur fulvus fulvus (brown lemur)
 C;Date: 30-Sep-1979 #sequence_revision 30-Sep-1979 #text_change 31-Mar-2000
 C;Accession: A02370
 R;Maita, T.; Setoguchi, M.; Matsuda, G.; Goodman, M.
 J. Biochem. 85, 755-764, 1979
 A;Title: Amino acid sequences of the alpha and beta chains of adult hemoglobin of the brown lemur
 A;Reference number: A91552; MUID:79150872
 A;Accession: A02370
 A;Molecule type: protein
 A;Residues: 1-146 <MAI>
 C;Superfamily: globin; globin homology <GLB>
 F;3-146/Domain: globin homology <GLB>
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;
 Qy 1 LVVVFWTQRF 10
 Db 32 LVVVFWTQRF 41
 RESULT 65
 HBLEC
 hemoglobin beta chain - ring-tailed lemur
 C;Species: Lemur catta (ring-tailed lemur)
 C;Date: 18-Aug-1982 #sequence_revision 17-Mar-1987 #text_change 03-Mar-2000
 C;Accession: A02371
 R;Copenhagen, D.H.; Dixon, J.D.; Duffy, L.K.
 Hemoglobin 7, 1-14, 1983
 A;Title: Prosimian hemoglobins I. The primary structure of the beta-globin chain of Lemur catta
 A;Reference number: A02371; MUID:3185437
 A;Accession: A02371
 A;Molecule type: protein
 A;Residues: 1-146 <COP>
 A;Note: residues 125-131 were positioned by homology
 C;Superfamily: globin; globin homology <GLB>
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F;3-146/Domain: globin homology <GLB>
 F;92/Binding site: oxygen (His) (distal axial ligand) #status predicted
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;
 Qy 1 LVVVFWTQRF 10
 Db 32 LVVVFWTQRF 41
 RESULT 66
 HBRTNG
 hemoglobin beta chain - northern gundi
 C;Species: Ctenodactylus gundi (northern gundi)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Mar-2000
 C;Accession: S13283; C33082
 R;Beintema, J.J.; Rodewald, K.; Braunitzer, G.
 Biol. Chem. Hoppe-Seyler 371, 1089-1099, 1990
 A;Title: The primary structures of gundi (Ctenodactylus gundi, Rodentia) hemoglobin a
 A;Reference number: S13282; MUID:91197427
 A;Accession: S13283
 A;Molecule type: protein
 A;Residues: 1-146

 C;Superfamily: globin; globin homology <GLB>
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F;3-146/Domain: globin homology <GLB>
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;
 Qy 1 LVVVFWTQRF 10
 Db 32 LVVVFWTQRF 41
 RESULT 67
 HBRTNG
 hemoglobin beta chain - northern gundi
 C;Species: Ctenodactylus gundi (northern gundi)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Mar-2000
 C;Accession: S13283; C33082
 R;Beintema, J.J.; Rodewald, K.; Braunitzer, G.
 Biol. Chem. Hoppe-Seyler 371, 1089-1099, 1990
 A;Title: The primary structures of gundi (Ctenodactylus gundi, Rodentia) hemoglobin a
 A;Reference number: S13282; MUID:91197427
 A;Accession: S13283
 A;Molecule type: protein
 A;Residues: 1-146

 C;Superfamily: globin; globin homology <GLB>
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F;3-146/Domain: globin homology <GLB>
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;
 Qy 1 LVVVFWTQRF 10
 Db 32 LVVVFWTQRF 41
 RESULT 68
 HBRR
 hemoglobin beta chain - raccoon
 C;Species: Procyon lotor (raccoon)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 C;Accession: S06525
 R;Brimhall, B.; Stangland, K.; Jones, R.T.; Becker, R.R.; Bailey, T.J.
 Hemoglobin 2, 351-370, 1978
 A;Title: Amino acid sequence of the hemoglobin of raccoon (Procyon lotor).
 A;Reference number: S06524; MUID:79026831
 A;Accession: S06525
 A;Molecule type: protein
 A;Residues: 1-146

 C;Superfamily: globin; globin homology <GLB>
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F;3-146/Domain: globin homology <GLB>
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;
 Qy 1 LVVVFWTQRF 10
 Db 32 LVVVFWTQRF 41
 RESULT 69
 HBBRT
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;
 Qy 1 LVVVFWTQRF 10
 Db 32 LVVVFWTQRF 41

hemoglobin beta chain - Asiatic black bear
 C;Species: Ursus tibetanus (Asiatic black bear)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Mar-2000
 C;Accession: A90709
 R;Hofmann, O.; Schreitmüller, T.; Braunitzer, G.; Wiesner, M.V.H.
 Biol. Chem. Hoppe-Seyler 367, 53-59, 1986
 A;Title: The primary structure of polar bear (*Ursus maritimus*, Carnivora) and Asiatic bl
 A;Reference number: A90709; MUID:86159301
 A;Accession: K90709
 A;Molecule type: protein
 A;Residues: 1-146 <HOF>
 A;Note: article in German with English abstract
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F;3-146/Domain: globin homology <GLB>
 F;92/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 70

HBMR hemoglobin beta chain - polar bear

C;Species: Ursus maritimus (polar bear)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Mar-2000
 C;Accession: B25880

R;Hofmann, O.; Schreitmüller, T.; Braunitzer, G.; Wiesner, M.V.H.
 Biol. Chem. Hoppe-Seyler 367, 53-59, 1986
 A;Title: The primary structure of polar bear (*Ursus maritimus*, Carnivora) and Asiatic bl
 A;Reference number: A90709; MUID:86159301
 A;Accession: B25880
 A;Molecule type: protein
 A;Residues: 1-146 <HOF>
 A;Note: article in German with English abstract
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F;3-146/Domain: globin homology <GLB>
 F;92/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 72

HBQG hemoglobin beta chain - giant panda
 C;Species: Ailuropoda melanoleuca (giant panda)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 C;Accession: S06529
 R;Pagle, D.A.; Miyamoto, M.M.; Goodman, M.; Hofmann, O.; Braunitzer, G.; Goeltenboch,
 Naturwissenschaften 73, 512-514, 1986
 A;Title: Hemoglobin of Pandas: phylogenetic relationships of carnivores as ascertained
 A;Reference number: S06526; MUID:87014854
 A;Accession: S06529
 A;Molecule type: protein
 A;Residues: 1-146 <TAG>
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F;3-146/Domain: globin homology <GLB>
 F;92/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 73

HBMN hemoglobin beta chain - domestic ferret
 C;Species: Mustela putorius furo (domestic ferret)

C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 03-Mar-2000
 C;Accession: S11534
 R;Pauplin, Y.; Hombrados, I.; Faure, F.; Han, K.K.; Neuzil, E.
 Biochem. Soc. Trans. 16, 608-609, 1988

A;Title: The primary structure of the beta-chain of the haemoglobins of the ferret (M
 A;Reference number: S11534
 A;Accession: S11534

A;Molecule type: protein
 A;Residues: 1-145 <PNT>
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F;3-146/Domain: globin homology <GLB>
 F;92/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 74

HRQL hemoglobin beta chain - lesser panda
 C;Species: Ailurus fulgens (lesser panda)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 C;Accession: S06527
 R;Tagle, D.A.; Miyamoto, M.M.; Goodman, M.; Hofmann, O.; Braunitzer, G.; Goeltenboch, R.
 Naturwissenschaften 73, 512-514, 1986
 A;Title: Hemoglobin of pandas: phylogenetic relationships of carnivores as ascertained w
 A;Reference number: S06526; MUID:87014854
 A;Accession: S06527
 A;Molecule type: protein
 A;Residues: 1-146 <TAG>
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein

HBOTE
hemoglobin beta chain - Eurasian river otter
C;Species: Lutra lutra (Eurasian river otter)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 03-Mar-2000
C;Accession: S00817
R;Lin, H.X.; Kleinschmidt, T.; Braunitzer, G.; Scheil, H.G.
R;Biol. Chem. Hoppe-Seyler 369, 349-355, 1988
A;Title: Carnivora: the primary structure of the common otter (Lutra lutra, Mustelidae)
A;Reference number: S00816; MUID: 89000194
A;Accession: S00817
A;Molecule type: protein
A;Residues: 1-146 <LIN>
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F;3-146/Domain: globin homology <GLB>
F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match	100.0%	Score 10;	DB 1;	Length 146;
Best Local Similarity	100.0%	Pred. No.	0.00017;	Indels 0;
Matches	10;	Mismatches	0;	Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 75

HBOTG
hemoglobin beta chain - giant otter
C;Species: Pteronura brasiliensis (giant otter)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C;Accession: S02081
R;Kleinschmidt, T.; Braunitzer, G.; Scheil, H.G.
Biol. Chem. Hoppe-Seyler 370, 35-40, 1989
A;Title: Carnivora: the primary structure of the giant otter (Pteronura brasiliensis, Mu
A;Reference number: S02080; MUID: 89228546
A;Accession: S02081
A;Molecule type: protein
A;Residues: 1-146 <KLE>
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F;3-146/Domain: globin homology <GLB>
F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match	100.0%	Score 10;	DB 1;	Length 146;
Best Local Similarity	100.0%	Pred. No.	0.00017;	Indels 0;
Matches	10;	Mismatches	0;	Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 76

HBDR
hemoglobin beta chain - ratel
C;Species: Mellivora capensis (ratel)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C;Accession: S01663
R;Rodewald, R.; Braunitzer, G.; Goelttenboth, R.
Biol. Chem. Hoppe-Seyler 369, 1137-1142, 1988
A;Title: Carnivora: primary structure of the hemoglobins from ratel (Mellivora capensis)
A;Reference number: S01662; MUID: 89207098
A;Accession: S01663
A;Molecule type: protein
A;Residues: 1-146 <PROD>
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F;3-146/Domain: globin homology <GLB>
F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match	100.0%	Score 10;	DB 1;	Length 146;
Best Local Similarity	100.0%	Pred. No.	0.00017;	Indels 0;
Matches	10;	Mismatches	0;	Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 79

HBDBM

F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

C;Species: Martes foina (beech marten)

C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 03-Mar-2000

C;Accession: S10599

R;Ruecknagel, K.P.; Wiesner, H.; Braunitzer, G.

Biol. Chem. Hoppe-Seyler 371, 503-509, 1990

A;Title: Carnivora: the primary structure of the beech marten (*Martes foina*, Mustelidae)

A;Reference number: S10598; MUID:9035058

A;Accession: S10599

A;Molecule type: protein

A;Residues: 1-16 <BIO>

C;Superfamily: globin; globin homology

C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein

F;3-146/Domain: globin homology <GLB>

F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146; Best Local Similarity 100.0%; Pred. No. 0.00017; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 LVVYPWTQRF 10 Db 32 LVVYPWTQRF 41

RESULT 80

HBW

hemoglobin beta chain - Pacific walrus

C;Species: *Odobenus rosmarus divergens* (Pacific walrus)

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000

C;Accession: S02820

R;Lin, H.X.; Kleinschmidt, T.; Johnson, M.L.; Braunitzer, G.

Biol. Chem. Hoppe-Seyler 370, 151-140, 1989

A;Title: Carnivora: the primary structure of the Pacific walrus (*Odobenus rosmarus divergens*)

A;Reference number: S02819; MUID:89207123

A;Accession: S02820

A;Molecule type: protein

A;Residues: 1-146 <LIN>

C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein

F;3-146/Domain: globin homology <GLB>

F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146; Best Local Similarity 100.0%; Pred. No. 0.00017; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 LVVYPWTQRF 10 Db 32 LVVYPWTQRF 41

RESULT 81

HBW

hemoglobin beta chain - Weddell seal

C;Species: *Leptonychotes weddelli* (Weddell seal)

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000

C;Accession: S04952

R;Lin, H.; Kleinschmidt, T.; Braunitzer, G.; Scheil, H.G.

Biol. Chem. Hoppe-Seyler 370, 707-713, 1989

A;Title: Carnivora: the primary structure of Weddell seal (*Leptonychotes weddelli*, PI)

A;Reference number: S04951; MUID:89374816

A;Accession: S04952

A;Molecule type: protein

A;Residues: 1-146 <LIN>

C;Superfamily: globin; globin homology

C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein

F;3-146/Domain: globin homology <GLB>

F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146; Best Local Similarity 100.0%; Pred. No. 0.00017; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 LVVYPWTQRF 10 Db 32 LVVYPWTQRF 41

RESULT 83

HBDD

hemoglobin beta chain - bottle-nosed dolphin

C;Species: *Tursiops truncatus* (bottle-nosed dolphin)

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000

C;Accession: S06523

R;Kleinschmidt, T.; Braunitzer, G.

Biomed. Biochim. Acta 42, 685-695, 1983

A;Title: The primary structure of the bottlenosed dolphin (*Tursiops truncatus*, cetacean)

A;Reference number: S06522; MUID:84052510

A;Accession: S06523

A;Molecule type: protein

A;Residues: 1-146 <RLK>

A;Note: article in German with English abstract

C;Superfamily: globin; globin homology

C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein

F;3-146/Domain: globin homology <GLB>

F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146; Best Local Similarity 100.0%; Pred. No. 0.00017; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 LVVYPWTQRF 10 Db 32 LVVYPWTQRF 41

RESULT 84

HBWHR

hemoglobin beta chain - minke whale F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 C;Species: Balaeoptera acutorostrata (minke whale, lesser rorqual)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 C;Accession: S06521
 R;Abbas, A.; Rucknagel, P.; Matsuda, G.; Zaidi, Z.H.; Braunitzer, G.
 J.Chem. Soc. Pak. 6, 253-256, 1984
 A;Title: The primary structure of Minke-whale (Balaeoptera acutorostrata - Cetacea) hemoglobin beta chain - minke whale
 A;Reference number: S06520
 A;Residues: 1-146 <ABB>
 A;Molecule type: protein
 A;Note: 72-Ala, 87-Ala, 123-Leu, and 128-Ser were also found
 C;Superfamily: globin; globin homology
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F:3-145/Domain: globin homology <GLB>
 F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 85

HBRY hemoglobin beta chain - false vampire bat (Megaderma lyra)

C;Species: Megaderma lyra
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 C;Accession: S00541
 A;Molecule type: protein
 A;Residues: 1-146 <SGO>
 C;Superfamily: globin; globin homology <GLB>
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F:3-146/Domain: globin homology <GLB>
 F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 87

HBDP hemoglobin beta chain - Amur leopard

C;Species: Panthera pardus orientalis (Amur leopard)
 C;Date: 04-Dec-1996 #sequence_revision 04-Dec-1996 #text_change 03-Mar-2000
 C;Accession: A02373
 R;Abbas, A.; Braunitzer, G.
 J. Protein Chem. 4, 57-67, 1985
 A;Title: The primary structure of haemoglobin from amur-leopard (Panthera pardus orie
 A;Reference number: A02377
 A;Molecule type: protein
 A;Residues: 1-146 <ABB>
 C;Comment: In the cat family (Felidae), the oxygen affinity of hemoglobin depends lit
 C;Superfamily: globin; globin homology <GLB>
 C;Keywords: acetylated amino end; blood; chromoprotein; erythrocyte; heme; iron; meta
 F:3-146/Domain: globin homology <GLB>
 F:63/Binding site: acetylated amino end (Ser) #status experimental
 F:92/Binding site: oxygen (His) (distal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 88

HBPP2P hemoglobin beta-II chain - northern Persian leopard

C;Species: Panthera pardus saxicolor (northern Persian leopard)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 C;Accession: S03929
 R;Ahmed, A.; Jahani, M.; Braunitzer, G.; Goeltzenboth, R.
 Z. Naturforsch. B 43, 1341-1346, 1988
 A;Title: Carnivore: the primary structure of the major and minor hemoglobin component
 A;Reference number: S03927
 A;Accession: S03929
 A;Molecule type: protein
 A;Residues: 1-146 <AHM>
 C;Superfamily: globin; globin homology <GLB>
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F:3-145/Domain: globin homology <GLB>
 F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 89
HBTL2
hemoglobin beta-II chain - lion
C;Species: Panthera leo (lion)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C;Accession: S03926
R;Jahan, M.; Ahmed, A.; Braunitzer, G.; zaidi, Z.H.; Goeltenboth, R.
Z. Naturforsch. B 42, 1465-1470, 1987
A;Title: Carnivora: the primary structures of adult lion (*Panthera leo*) hemoglobins.
A;Reference number: S03924
A;Accession: S03926
A;Molecule type: protein
A;Residues: 1-146 <R>
C;Superfamily: globin; globin homology
C;Keywords: acetylated amino end; blood; chromoprotein; erythrocyte; heme; heterotetr
F;3-146/Domain: globin homology <GLB>
F;1/Modified site: acetylated amino end (Ser) #status experimental
F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted
F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10
Db 32 LVVYPTQRF 41

RESULT 90
HBJU
hemoglobin beta-I chain - jaguar
C;Species: Panthera onca (Jaguar)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 03-Mar-2000
C;Accession: S00522
R;Ahmed, A.; Jahan, M.; zaidi, Z.H.; Braunitzer, G.; Goeltenboth, R.
Z. Naturforsch. B 42, 1465-1470, 1987
A;Title: Carnivora: the primary structures of adult lion (*Panthera leo*) hemoglobins.
A;Reference number: S00521; MUID: 88107004
A;Accession: S00522
A;Molecule type: protein
A;Residues: 1-146 <R>
A;Note: the sequence of the beta-II chain differs from that shown in having 1-Gly and 13
C;Superfamily: globin; globin homology
C;Keywords: acetylated amino end; blood; chromoprotein; erythrocyte; heme; heterotetra
F;3-146/Domain: globin homology <GLB>
F;1/Modified site: acetylated amino end (Ser) #status experimental
F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10
Db 32 LVVYPTQRF 41

RESULT 92
HBTL1
hemoglobin beta-I chain - lion
C;Species: Panthera leo (lion)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C;Accession: S03925
R;Jahan, M.; Ahmed, A.; Braunitzer, G.; zaidi, Z.H.; Goeltenboth, R.
Z. Naturforsch. B 42, 1465-1470, 1987
A;Title: Carnivora: the primary structures of adult lion (*Panthera leo*) hemoglobins.
A;Reference number: S03924
A;Accession: S03925
A;Molecule type: protein
A;Residues: 1-146 <R>
A;Note: the sequence of the beta-II chain differs from that shown in having 1-Gly and 13
C;Superfamily: globin; globin homology
C;Keywords: acetylated amino end; blood; chromoprotein; erythrocyte; heme; heterotetr
F;3-146/Domain: globin homology <GLB>
F;1/Modified site: acetylated amino end (Ser) #status experimental
F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10
Db 32 LVVYPTQRF 41

RESULT 93
HBDP1P
hemoglobin beta-I chain - northern Persian leopard
C;Species: Panthera pardus saxicolor (northern Persian leopard)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C;Accession: S03928
R;Ahmed, A.; Jahan, M.; Braunitzer, G.; Goeltenboth, R.
Z. Naturforsch. B 43, 1311-1316, 1988
A;Title: Carnivora: the primary structure of the major and minor hemoglobin component
A;Reference number: S03927
A;Accession: S03928
A;Molecule type: protein
A;Residues: 1-146 <R>
A;Note: the sequence of the beta-II chain differs from that shown in having 1-Gly and 13
C;Superfamily: globin; globin homology
C;Keywords: acetylated amino end; blood; chromoprotein; erythrocyte; heme; heterotetr
F;3-146/Domain: globin homology <GLB>
F;1/Modified site: acetylated amino end (Ser) #status experimental
F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10

Db 32 |||L^{VVY}PW^HO^RF 41
RESULT 94
 HBTX2
 hemoglobin beta-II chain - tiger
 C;Species: *Panthera tigris sumatrae* (Sumatran tiger)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 C;Accession: S11301
 R;Jahan, M.; Ahmed, A.; Braunitzer, G.; Goeltenboth, R.
 R;Chem. Hoppe-Seyler 370, 27-33, 1989
 A;Title: Carnivora: the amino-acid sequence of the adult Sumatran tiger (*Panthera tigris*)
 A;Reference number: S02078; MUID:89228545
 A;Molecule type: protein
 A;Residues: 1-146 <AHA>
 C;Superfamily: globin; globin homology <GLB>
 F;3-146/Domain: globin homology <GLB>
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 L^{VVY}PW^HO^RF 10
 Db 32 |||L^{VVY}PW^HO^RF 41
RESULT 95
 HBTF
 hemoglobin beta chain - Egyptian rousette (tentative sequence)
 C;Species: *Rousettus aegyptiacus* (Egyptian rousette)
 C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 31-Mar-2000
 C;Accession: A02376
 R;Klein Schmidt, T.; Braunitzer, G.
 R;Hoppe-Seyler, Z. Physiol. Chem. 363, 1209-1215, 1982
 A;Title: Die Primärstruktur des Hämoglobins vom Ägyptischen Flughund (*Rousettus aegyptiacus*)
 A;Reference number: A91702; MUID:83055089
 A;Accession: A02376
 A;Molecule type: protein
 A;Residues: 1-146 <KIE>
 C;Superfamily: globin; globin homology <GLB>
 F;3-146/Domain: globin homology <GLB>
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 L^{VVY}PW^HO^RF 10
 Db 32 |||L^{VVY}PW^HO^RF 41
RESULT 96
 HBFB
 hemoglobin beta chain - black flying fox
 C;Species: *Pteropus alecto* (black flying fox)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
 C;Accession: S01309
 R;Klein Schmidt, T.; Sgouras, J.G.; Pettigrew, J.D.; Braunitzer, G.
 R;Biol. Chem. Hoppe-Seyler 369, 975-984, 1988
 A;Title: The primary structure of the hemoglobin from the grey-headed flying fox (Pteropus alecto)
 A;Reference number: S01309; MUID:89149963
 A;Accession: S01311
 A;Molecule type: protein
 A;Residues: 1-146 <KIE>
 A;Note: 139-Thr was also found
 C;Superfamily: globin; globin homology <GLB>
 F;3-146/Domain: globin homology <GLB>
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 L^{VVY}PW^HO^RF 10
 Db 32 |||L^{VVY}PW^HO^RF 41
RESULT 98
 HBHH
 hemoglobin beta chain - western European hedgehog (tentative sequence)
 C;Species: *Erinaceus europaeus* (western European hedgehog)
 C;Date: 30-Jun-1979 #sequence_revision 30-Jun-1979 #text_change 31-Mar-2000
 C;Accession: A02377
 R;Maita, T.; Araya, A.; Matsuda, G.; Goodman, M.
 J. Biochem. 85, 259-269, 1979
 A;Title: Amino acid sequences of the alpha and beta chains of adult hemoglobin of the western European hedgehog (*Erinaceus europaeus*)
 A;Reference number: A91950; MUID:79109529
 A;Accession: A02377
 A;Molecule type: protein
 A;Residues: 1-146 <MAI>
 C;Superfamily: globin; globin homology <GLB>
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F;3-146/Domain: globin homology <GLB>
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVVPTQRF 10
 |||||||
 Db 32 LVVVPTQRF 41

RESULT 99

HBSTM

hemoglobin beta chain - house shrew (tentative sequence)

C;Species: Suncus murinus (house shrew)

C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 31-Mar-2000

C;Accession: A02378

R;Maita, T.; Matsuda, G.; Takenaka, O.; Takahashi, K.

HOPPE-Seyler's Z. Physiol. Chem. 362, 1465-1474, 1981

A;Title: The primary structure of adult hemoglobin of musk shrew (Suncus murinus).

A;Reference number: A91699; MUID:02074278

A;Accession: A02378

A;Molecule type: protein

A;Residues: 1-146 <MAID>

C;Superfamily: globin; globin homology

C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F;3-146/domain: globin homology <GLOB>

F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVVPTQRF 10
 |||||||
 Db 32 LVVVPTQRF 41

RESULT 100

HBSE

hemoglobin beta chain - European mole (tentative sequence)

C;Species: Talpa europaea (European mole)

C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 31-Mar-2000

C;Accession: A02379

R;Kleinschmidt, T.; Jelkmann, W.; Braunitzer, G.

HOPPE-Seyler's Z. Physiol. Chem. 362, 1263-1272, 1981

A;Title: Die primärstruktur des Haemoglobins des Maulwurfs (Talpa europaea).

A;Reference number: A91697; MUID:82263326

A;Accession: A02379

A;Molecule type: protein

A;Residues: 1-146 <KLE>

C;Superfamily: globin; globin homology

C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F;3-146/domain: globin homology <GLOB>

F;63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F;92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVVPTQRF 10
 |||||||
 Db 32 LVVVPTQRF 41

Search completed: July 1, 2002, 12:07:10
 Job time: 43 sec

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OM protein - protein search, using sw model

Run on: July 1, 2002, 12:07:12 ; Search time 10.33 Seconds
 (without alignments)
 37.483 M.illion cell updates/sec

Title: US-09-147-490-1
 perfect score: 10
 Sequence: 1 LVVYPWTORF 10

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues
 Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

post-processing: Listing first 100 summaries

Database : SwissProt_40;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	100.0	60	1 HBB_MACEU	P81042 macropus eu
2	100.0	141	1 HBBG_SHEEP	P02078 capra hircu
3	100.0	141	1 HBBB_BOSDA	P02079 ovis aries
4	100.0	145	1 HBBA_CAPIT	P04346 bos Javanic
5	100.0	145	1 HBBC_BOVIN	P02077 capra hircu
6	100.0	145	1 HBBF_CAPIT	P02081 bos taurus
7	100.0	145	1 HBBG_SHEEP	P02082 capra hircu
8	100.0	145	1 HBB_ALCAA	P02083 ovis aries
9	100.0	145	1 HBB_BISBO	P02073 alces alces
10	100.0	145	1 HBB_BOVIF	P09422 bison bonas
11	100.0	145	1 HBB_BOSMU	P02071 bos gaurus
12	100.0	145	1 HBB_BOVIN	P02072 bos mutus g
13	100.0	145	1 HBB_ODOVI	P02070 bos taurus
14	100.0	145	1 HBBL_SPHEU	P02074 odocoileus
15	100.0	145	1 HBB_OVIMO	P02076 ovis orient
16	100.0	145	1 HBB_RANTA	P21380 rangifer ta
17	100.0	145	1 HBB_SHEEP	P02075 ovis aries
18	100.0	145	1 HBB_TRAST	P04245 tragelaphus
19	100.0	146	1 HBBL_IGUIG	P18987 iguana iguana
20	100.0	146	1 HBBL_SPHEU	P00060 sphenodon p
21	100.0	146	1 HBBI_TAPPE	P02064 tapirus ter
22	100.0	146	1 HBBI_UROHIA	P18991 uromystyx h
23	100.0	146	1 HBB2_PANIE	P18988 panthera le
24	100.0	146	1 HBB2_TAPPE	P02065 tapirus ter
25	100.0	146	1 HBB_AILFU	P18982 ailurus ful
26	100.0	146	1 HBB_AILME	P18983 ailuropoda
27	100.0	146	1 HBB_ANTPA	P14388 antrozous p
28	100.0	146	1 HBB_AOTTR	P02035 atetus trivi
29	100.0	146	1 HBB_ATEGE	P02034 atelus geoff
30	100.0	146	1 HBB_BALAC	P18984 balanopter
31	100.0	146	1 HBB_CALPAR	P18985 callithrix
32	100.0	146	1 HBB_CAVPO	P02095 cavia porce
33	100.0	146	1 HBB_CEBAL	P02040 cebus albif

RESULT 1

ALIGNMENTS

P02041	cebush apell
P02028	cercopithec
P02066	ceratotheri
P02031	cercocebus
P02033	colobus bad
P18985	colobus pol
P18986	crocata cro
P02085	ctenodactyl
P11754	cynopterus
P02087	dassipus nov
P24292	echinops te
P02063	equus hemio
P02059	erinaceus e
P02053	eulemur ful
P02025	hylobates l
P02054	lemur catta
P21667	lemur varie
P08535	lepus europ
P15166	leptonychot
P02048	loris tard
P10893	lutra lutra
P1328	lynx lynx (
P09840	macrotus ca
P02027	macaca fusc
P24660	macrourus
P08259	mandrillus
P08853	marmota mar
P11752	megaderma l
P15449	melillivora c
P23602	mesocricetus
P23607	mustela lut
P11758	myotis vell
P25916	nasua nasua
P02049	nycticebus
P10779	odobenus ro
P02093	ondatra zib
P02011	ornithorhynch
P19646	paguma larv
P04244	panthera pa
P10884	panthera ti
P02030	papio cyno
P09909	phoca vitul
P05905	physaster ca
P02067	sus scrofa
P02032	presbytis e
P23020	proteles cr
P02086	procavia ca
P18989	procyon lot
P14391	pteropus al
P10886	pteropus b
P14392	pteropus po
P02057	oryctolagus
P09907	rhinoceros
P02058	rousettus a
P02039	saguinus fu
P02038	saguinus my
P02037	saguinus ni
P02036	saimiri sci
P02090	spalax leuc
P09421	spermophilu

HBE_MACEU
ID HBE_MACEU STANDARD; PRT; 60 AA.
AC P81042;
DT 15-JUL-1998 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Hemoglobin epsilon chain (Fragment).
GN HBEL.
OS Macropus eugenii (Tanner wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
NCBI_TaxID=9315;
RN [1]
RP SEQUENCE:
RC TISSUE=Blood;
RX MEDLINE=98000287; PubMed=9342240;
RA Holland R.A.B.; Gooley A.A.;
RT "Characterization of the embryonic globin chains of the marsupial
Tanner wallaby, *Macropus eugenii*,";
EUR. J. Biochem. 248:864-871(1997).
CC -I- FUNCTION: HEMOGLOBIN EMBRYONIC CHAIN IS A EMBRYONIC-TYPE BETA-TYPE
CHAIN FOUND IN PRENATAL AND NEONATAL MARSUPIALS.
DR HSSP; P02100; IANW.
DR Interpro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PROSITE; PS0103; GLOBIN; 1.
DR Heme; Oxygen transport; Transport; Erythrocyte.
KW NON_TER 60
FT SEQUENCE 60 AA; 6510 MW; C3CF20BC445C649C CRC64;

RESULT 2
HBBC_CAPHT
ID HBBC_CAPHT STANDARD; PRT; 141 AA.
AC P02078;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta-C chain (Cysteine-beta).
OS *Capra hircus* (goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8213705; PubMed=6277503;
RA Schon E.A., Cleary M.L., Haynes J.R., Lingrel J.B.,
RT "structure and evolution of goat gamma-, beta C- and beta A-globin
genes: three developmentally regulated genes contain inserted
elements.,";
RT Cell 27:359-369(1981).
-I- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
VARIOUS PERIPHERAL TISSUES.
-I- SUBUNIT: HEMOGLOBIN OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
-I- TISSUE SPECIFICITY: RED BLOOD CELLS.
-I- MISCELLANEOUS: THIS TYPE OF BETA-C CHAIN IS FOUND WHEN ANEMIA HAS
BEEN EXPERIMENTALLY PRODUCED.
-I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

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CC CC CC CC
DR DR DR DR
DR PIR; A02396; HGTC.
DR HSSP; P02070; LHDA.
DR Interpro; IPR002337; Beta_haem.
DR Interpro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINS; PRO0814; BEPAHAE.
DR PROSITE; PS0103; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT INIT_MET 0 IRON (HEME DISTAL LIGAND).
FT METAL 58 58 IRON (HEME PROXIMAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 141 AA; 15620 MW; 305CEA482FAC825C CRC64;

RESULT 3
HBBC_SHEEP
ID HBBC_SHEEP STANDARD; PRT; 141 AA.
AC P02C19;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-JUN-1994 (Rel. 20, Last annotation update)
DE Hemoglobin beta-C chain.
OS *Ovis aries* (Sheep),
OS *Ovis orientalis musimon* (Mouflon), and
OS *Ammotragus lervia* (Barbary sheep) (Aoudad).
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis;
OC NCBI_TaxID=9940; 9938; 9899;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Sheep;
RX MEDLINE=8917874; PubMed=2494347;
RA Garner K.J., Lingrel J.B.;
RT "A comparison of the beta A-and beta B-globin gene clusters of
sheep";
RT Mol. Evol. 28:175-184(1989).
RL J. Mol. Evol. 28:175-184(1989).
RN [2]
RP SEQUENCE.
RC SPECIES=Sheep;
RX MEDLINE=67134317; PubMed=6022868;
RA Boyer S.H., Hathaway P., Pascasio F., Bordley J., Orton C.,
RA Naughton M.A.;
RT "Differences in the amino acid sequences of tryptic peptides from
three sheep hemoglobin beta chains.,";
RT J. Biol. Chem. 242:2211-2232(1967).
RN [3]
RP SEQUENCE.
RC SPECIES=Sheep;
RA Wilson J.B., Edwards W.C., McDaniel M., Dobbs M.M., Huisman T.H.J.;
RT "The structure of sheep hemoglobins. II. The amino acid composition
of the tryptic peptides of the non-alpha chains of hemoglobins A, B,
C, and F.,";
RT C. and F.;
RL Arch. Biochem. Biophys. 115:385-400(1966).
[4]
RP COMPOSITION OF TRYPTIC PEPTIDES EXCEPT POSITIONS 100-111.
RC SPECIES=O. musimon, and A. lesvia;
RX MEDLINE=7108922; PubMed=5496330;
RA Wilson J.B., Miller A., Huisman T.H.J.;

RT "Production of hemoglobin C in the Moufflon (*Ovis musimon* Pallas, 1811) and the Barbery sheep (*Ammotragus lervia* Pallas, 1777) during experimental anemia; amino acid composition of tryptic peptides from the beta B and bet C chains.";

RL Biochem. Genet. 4:677-688(1970).

CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.

CC -!- SUBUNIT: HETEROOTERAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC -!- MISCELLANEOUS: THIS TYPE OF BETA-C CHAIN IS FOUND IN THESE ANIMALS WHEN ANEMIA HAS BEEN EXPERIMENTALLY PRODUCED.

CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

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CC

DR EMBL; X14728; CAA32850.1; -.

DR PIR; A02396; HBSC.

DR PIR; A02396; HBSC.

DR PIR; S10074; S10074.

DR InterPro; IPR002337; Beta_haem.

DR InterPro; IPR00571; Globin.

DR PRINTS; PRO0814; BETAHAE.

DR PROSITE; PS01033; GLOBIN; 1.

DR Heme; Oxygen transport; Transport; erythrocyte.

FT INIT_MET 0 0

FT METAL 58 58 IRON (HEME DISTAL LIGAND).

FT VARIANT 68 68 IRON (HEME PROXIMAL LIGAND).

FT CONFLICT 82 82 N -> Z (IN BARBARY SHEEP). Q -> E (IN REF. 3).

SQ SEQUENCE 141 AA; 15619 MW; 3409EDB54528C358 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 145; Best Local Similarity 100.0%; Pred. No. 4.1e-05; Mismatches 0; Indels 0; Gaps 0; Matches 10; Conservative 0; MisMatches 0; PIR; A02396; HBSC.

Db 31 LVVYPWTQRF 10

RESULT 5

ID HBBA_CAPII STANDARD; PRT; 145 AA.

ID HBBA_CAPII

AC P02077;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Hemoglobin beta-A chain (Alanine-beta).

OS Capra hircus (Goat).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Capra.

OX NCBI_TaxID:995;

RN [1]

RP SOURCE FROM N.A.

RX MEDLINE=8213705; PubMed=6277503;

RA Schon E.A., Cleary M.L., Haynes J.R., Lingrel J.B.;

RT "Structure and evolution of goat gamma-, beta C- and beta A-globin genes: three developmentally regulated genes contain inserted elements.";

RT Cell 27:359-369(1981).

RL RN [2]

RP PARTIAL SEQUENCE (ALLELE A).

RX MEDLINE=67165362; PubMed=6026247;

RA Huisman T.H.J., Adams H.R., Dimmock M.O., Edwards W.E., Wilson J.B.;

RT "The structure of goat hemoglobins. I. Structural studies of the beta chains of the hemoglobins of normal and anemic goats.";

RL J. Biol. Chem. 242:2534-2541(1967).

RN [3]

RP PARTIAL SEQUENCE (ALLELE D).

RX MEDLINE=69016192; PubMed=6697993;

RA Adams H.R., Boyd E.M., Wilson J.B., Miller A., Huisman T.H.J.;

RT "The structure of goat hemoglobins. 3. Hemoglobin D, a beta A-chain variant with one apparent amino acid substitution (21 Asp-->His).";

RT Wrightstone R.N., Wilson J.B., Miller A., Huisman T.H.J.;

RL Arch. Biochem. Biophys. 127:398-405(1968).

RN [4]

RP PARTIAL SEQUENCE (ALLELE E).

RX MEDLINE=70252721; PubMed=5433580;

RA Wrightstone R.N., Wilson J.B., Miller A., Huisman T.H.J.;

RT "The structure of goat hemoglobins. IV. A third beta chain variant (betae) with three apparent amino acid substitutions.";

RL Arch. Biochem. Biophys. 138:451-456(1970).

CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.

CC -!- SUBUNIT: HETEROOTERAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC -!- POLYMORPHISM: THERE ARE AT LEAST ALLELES. THE SEQUENCE SHOWN IS

RT Nambu T., Takenaka O., Takahashi K.; "Hemoglobin Ball (bovine); beta A 18(B1)lys leads to His: one of the missing links' between beta A and beta B of domestic cattle exists in the Ball cattle (Bovinae, Box banteng)." ; Biochem. Genet. 21:787-796(1983).

RT -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.

CC THAT OF ALLELE A.
 CC -! SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
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 EMBL; M15387; AAA30913; ; -.
 DR PIR; A02195; HBGTA.
 DR HSSP; P0070; IHDA.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 KW Polymorphism.
 FT METAL 62 62 IRON (HEME DISTAL LIGAND).
 FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 20 20 D -> H (IN ALLELE D).
 FT VARIANT 86 86 Q -> H (IN ALLELE E).
 FT VARIANT 103 103 K -> R (IN ALLELE E).
 FT VARIANT 124 124 L -> V (IN ALLELE E).
 SQ SEQUENCE 145 AA; 16021 MW; 6C59F1059A40E4D0 CRC64;

Query Match Score 10; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVVPWTQRF 10
 Db 31 LVVVPWTQRF 40

RESULT 6

HBFB_BOVIN	STANDARD;	PRT;	145 AA.
HBFB_BOVIN			
AC P02081;			
DT 21-JUL-1986 (Rel. 01, created)			
DT 21-JUL-1986 (Rel. 01, last sequence update)			
DE Hemoglobin beta fetal chain (Hemoglobin gamma chain).			
OS Bos taurus (Bovine).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;			
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;			
OC Bovidae; Bovinae; Bos.			
NCBI_TAXID=9913;			
RN [1]			
SEQUENCE FROM N.A.			
RX MEDLINE=4144058; PubMed=6322113;			
RA Schimenti J.C., Duncan C.H.;			
RT "Ruminant globin gene structures suggest an evolutionary role for			
RT Alu-type repeats.", Nucleic Acids Res. 12:1641-1655(1984).			
RN [2]			
SEQUENCE.			
RX MEDLINE=67089183; PubMed=5958205;			
RA Babin D.R., Schroeder W.A., Shelton J.R., Shelton J.B., Robberson B.;			
RT "The amino acid sequence of the gamma chain of bovine fetal			
RT hemoglobin.", Biochemistry 5:1297-1310(1986).			
RN [3]			
SEQUENCE.			
RX MEDLINE=83005406; PubMed=7118074;			
RA Kleinschmidt T., Braunitzer G.;			
RT "The primary structure of the hemoglobin gamma-chains of fetal sheep			
(Ovis ammon) and goat (<i>Capra aegagrus</i>). Artiodactyla.", Roppe-Seyler's Z. Physiol. Chem. 363:789-796(1982).			
RN [4]			
SEQUENCE OF 52-97 FROM N.A.			
RX MEDLINE=8022776; PubMed=6248519;			
RA Haynes J.R., Rostock P.R., Schon E.A., Gallagher P.M., Burks D.J.,			
RA Smith K., Lingrel J.B.;			
RT "The isolation of the beta A-, beta C-, and gamma-globin genes and a			
RT presumptive embryonic gene from a goat DNA recombinant library.",			
RT J. Biol. Chem. 255:6355-6367(1980).			
RL -! FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE			
CC -! SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.			
CC -! SIMILARITY: BELONGS TO THE GLOBIN FAMILY.			

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 CC
 EMBL; X00354; CAA25101.1; -.
 DR EMBL; M6452; AAA30519.1; -.
 DR PIR; A02398; HBBOF.
 DR HSSP; P02070; IHDA.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPRO00971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 KW METAL 62 62 IRON (HEME DISTAL LIGAND).
 FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 145 AA; 15859 MW; 78B8722915EGC221 CRC64;

Query Match Score 10; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVVPWTQRF 10
 Db 31 LVVVPWTQRF 40

CC -----
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 CC -----
 DR EMBL; M15388; AAA30925.1; -.
 DR EMBL; K00663; AAA30923.1; -.
 DR PIR: A02399; HBGTF.
 DR HSSP; P03070; IHDA.
 DR InterPro; IPR002331; Beta_haem.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PR00814; BEPAHAEM.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT IRON (HEME DISTAL LIGAND).
 FT METAL 62 62 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 145 AA; 15946 MW; E143C91CC8989652 CRC64;
 DR -----
 Query Match 100:0%; Score 10; DB 1; Length 145;
 Best Local Similarity 100:0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR QY 1 LVVVPWTQRF 10
 DR |||||||
 DR 31 LVVVPWTQRF 40
 DR -----
 RESULT 8
 HBBF_SHEEP STANDARD: PRT: 145 AA.
 ID HBBF_SHEEP
 AC P02083;
 DT 21-JUL-1986 (Rel. 01, created)
 DT 01-JUN-1994 (Rel. 01, last sequence update)
 DT Hemoglobin beta fetal chain (Hemoglobin gamma chain).
 OS Ovis aries (Sheep).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Caprinae; Ovis.
 OX NCBI_TAXID=9940;
 RN [1] SEQUENCE OF 1-29; 52-96 AND 104-145 FROM N.A.
 RX MEDLINE=9117290; PubMed=6161931;
 RA Kreitschmer P.J., Coon H.C., Davis A., Harrison M., Nienhuis A.W.;
 RT "Hemoglobin switching in sheep. Isolation of the fetal gamma-globin
 gene and demonstration that the fetal gamma- and adult beta A-globin
 genes lie within eight kilobase segments of homologous DNA.";
 RT J. Biol. Chem. 256:1975-1982(1981).
 RN [2] SEQUENCE;
 RP MEDLINE=7022158; PubMed=974104;
 RA Darbre P.D., Lehmann H.;
 RT "The gamma chain of the lamb";
 RL Biophys. Acta 446:10-18(1976);
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 CC -----
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 or send an email to license@sb-sib.ch).
 CC -----
 DR EMBL; K02824; AAA31533.1; -.
 DR -----
 DR EMBL; K02826; AAA31535.1; -.
 DR PIR: A92306; HSH.
 DR HSSP; P03070; IHDA.
 DR InterPro; IPR002331; Beta_haem.
 DR PIR: IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PR00811; BEPAHAEM.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT IRON (HEME DISTAL LIGAND).
 FT METAL 62 62 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 145 AA; 15931 MW; 9924A27CCBC34C28 CRC64;
 DR -----
 Query Match 100:0%; Score 10; DB 1; Length 145;
 Best Local Similarity 100:0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR QY 1 LVVVPWTQRF 10
 DR |||||||
 DR 31 LVVVPWTQRF 40
 DR -----
 RESULT 9
 HBB_ALCAA STANDARD: PRT: 145 AA.
 ID HBB_ALCAA
 AC P02073;
 DT 21-JUL-1986 (Rel. 01, created)
 DT 21-JUL-1986 (Rel. 01, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Hemoglobin beta chain.
 OS Alces alces (European moose) (Elk).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
 OC Cervidae; Odocoileinae; Alces.
 OX NCBI_TAXID=9833;
 RP [1] SEQUENCE.
 RX MEDLINE=85078042; PubMed=6510898;
 RA Aschner H., Wiesner H., Braunitzer G.;
 RT "Intrinsic oxygen affinity: the primary structure of a ruminantia
 hemoglobin: methionine in beta₂ of a Pecora, the Northern elk
 (Alces alces alces)".
 RL Hoppe-Seyler's Z. Physiol. Chem. 355:1323-1330(1994).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02392; HBNK.
 DR HSSP; P02070; IHDA.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PR00814; BEPAHAEM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT IRON (HEME DISTAL LIGAND).
 FT METAL 62 62 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 145 AA; 16223 MW; C2D2F363D3B/8BA CRC64;
 DR -----
 Query Match 100:0%; Score 10; DB 1; Length 145;
 Best Local Similarity 100:0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR QY 1 LVVVPWTQRF 10
 DR |||||||
 DR 31 LVVVPWTQRF 40
 DR -----

RESULT 10

ID HBB_BISBO	STANDARD:	PRT; 145 AA.
AC P09422;		
DT 01-MAR-1989 (Rel. 10, Created)		
DT 01-MAR-1989 (Rel. 10, Last sequence update)		
DT 16-OCT-2001 (Rel. 40, Last annotation update)		
DE Hemoglobin beta chain.		
GN HBB.		
OS Bison bonasus (European bison).		
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bovidae; Bovinae; Bison.		
OC NEBI_TAXID=9902;		
RN [1]		
RP SEQUENCE.		
SQ MEDLINE=86296178; PubMed=3741621; Mazur G., Mueller E., Braunitzer G., Wiesner H.; "Intrinsic oxygen affinity of hemoglobins: the hemoglobin of bisons (Bison bonasus, Bovidae)."; Biol. Chem. Hoppe-Seyler 367:417-423(1986). -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.		
CC -1- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.		
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.		
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.		
PIR: C25727; C25727.		
DR InterPro; IPR002337; Beta_haem.		
DR Print; PF00042; globin_1.		
DR PROSITE; PS01033; GLOBIN_1.		
KW Heme; Oxygen transport; Transport; Erythrocyte.		
FT METAL 62 62 IRON (HEME DISTAL LIGAND).		
FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).		
FT SEQUENCE 145 AA; 15976 MW; 4634F52EC1772BA3 CRC64;		

Query Match 100.0%; Score 10; DB 1; Length 145; Best Local Similarity 100.0%; Pred. No. 4 2e-05; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10	DR 1111111111
Db 31 LVVYPWTQRF 40	

RESULT 11

ID HBB_BOSGF	STANDARD:	PRT; 145 AA.
AC P02071;		
DT 21-JUL-1986 (Rel. 01, Created)		
DT 21-JUL-1986 (Rel. 01, Last sequence update)		
DT 16-OCT-2001 (Rel. 40, Last annotation update)		
DE Hemoglobin beta chain.		
HBB.		
Bos gaurus frontalis (Gaya), and		
Bubalus bubalis (Domestic water buffalo).		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.		
OC NCBI_TAXID=30520, 89462;		
RN [1]		
RP SEQUENCE.		
RC SPECIES=g_frontalis;		
RA MEDLINE=85005246; PubMed=6479895;		
RA Lalithantluanga R., Wiesner H., Braunitzer G.; "Amino acid sequence of gayal hemoglobin (Bos gaurus frontalis, Bovidae)."; Hoppe-Seyler's Z. Physiol. Chem. 365:737-741(1984).		
RA Lalithantluanga R., Wiesner H., Braunitzer G.; "Studies on yak hemoglobin (Bos grunniens, Bovidae): structural basis for high intrinsic oxygen affinity?"; Biol. Chem. Hoppe-Seyler 366:63-68(1985).		
CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.		
CC -1- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.		
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.		
CC -1- POLYMORPHISM: THE BETA-II ALLELE IS SHOWN, IT OCCURS MUCH MORE FREQUENTLY THAN THE BETA-I ALLELE.		
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.		
DR PIR; AU2390; HBFA2.		
DR HSSP; P02070; IHD.		
DR InterPro; IPR002337; Beta_haem.		
DR Print; PF00042; globin_1.		
DR PROSITE; PS00814; BETAHAE.		
KW Heme; Oxygen transport; Transport; Erythrocyte;		

RESULT 12

ID HBB_BOSMU	STANDARD:	PRT; 145 AA.
AC P12072;		
DT 21-JUL-1986 (Rel. 01, Created)		
DT 16-OCT-2001 (Rel. 40, Last annotation update)		
DE Hemoglobin beta chain.		
HBB.		
Bos mutus grunniens (yak).		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.		
OC NCBI_TAXID=30521;		
RN [1]		
RP SEQUENCE (BETA-I AND BETA-II ALLELES).		
RA MEDLINE=85225945; PubMed=4005038;		
RA Lalithantluanga R., Wiesner H., Braunitzer G.; "Studies on yak hemoglobin (Bos grunniens, Bovidae): structural basis for high intrinsic oxygen affinity?"; Biol. Chem. Hoppe-Seyler 366:63-68(1985).		
CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.		
CC -1- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.		
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.		
CC -1- POLYMORPHISM: THE BETA-II ALLELE IS SHOWN, IT OCCURS MUCH MORE FREQUENTLY THAN THE BETA-I ALLELE.		
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.		
DR PIR; AU2390; HBFA2.		
DR HSSP; P02070; IHD.		
DR InterPro; IPR002337; Beta_haem.		
DR Print; PF00042; globin_1.		
DR PROSITE; PS00814; BETAHAE.		
KW Heme; Oxygen transport; Transport; Erythrocyte;		

CC	-1- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS
CC	WWW="http://www.worthington-biochem.com/manual/H/HB.html".
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-1- DATABASE: NAME=worthington_enzyme_manual;
CC	WWW="http://www.worthington-biochem.com/manual/H/HB.html".
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC	-1- POLYMORPHISM: FOUR ALLElic BETA CHAINS HAVE BEEN FOUND IN BOVINE HEMOGLOBINS. A AND B ALLELES WERE FOUND IN JERSEY CATTLE AND C AND D ALLELES WERE FOUND IN ANGOST CATTLE (EAST AFRICAN SHORT-HORN ZEBU). THE SEQUENCE SHOWN IS THAT OF THE ALLELE A.
CC	-1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
KW	Polymerism.
FT	METAL 62 62 IRON (HEME DISTAL LIGAND).
FT	METAL 91 91 IRON (HEME PROXIMAL LIGAND).
FT	VARIANT 49 49 S -> T (IN BETA-I ALLELE).
FT	VARIANT 116 116 H -> N (IN BETA-I ALLELE).
FT	VARIANT 134 134 V -> A (IN BETA-I ALLELE).
SQ	SEQUENCE 145 AA; 15951 MW; F937353DA65F4A2 CRC64;
RESULT	13
Query	Match
Best Local Similarity	100 %;
Matches	Score 10;
10	DB 1;
Conservative	Length 145;
0;	Pred. No. 4.2e-05;
0;	Mismatches 0;
0;	Indels 0;
0;	Gaps 0;
HBB_BOVIN	STANDARD;
ID	PRT; 145 AA.
AC	P02070;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)
DE	Hemoglobin beta chain.
HBB	Bovine.
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovine; Bos.
OC	NCBI_TAXID=9913;
RN	[1]
RP	SEQUENCE FROM N.A. (ALLELE A).
RA	MEDLINE=B1444058; PubMed=6322113;
RA	Schimenti J.C., Duncan C.H.;
RA	Ruminant globin gene structures suggest an evolutionary role for Alu-type repeats. ";
RA	Nucleic Acids Res. 12:1641-1655(1984).
RN	[2]
RP	SEQUENCE (ALLELES A AND B).
RX	MEDLINE=6001834; PubMed=6048711;
RA	Schreeder W.A., Shelton J.R., Shelton J.B., Robberson B., Babin D.R.;
RT	"A comparison of amino acid sequences in the beta-chains of adult bovine hemoglobins A and B.";
RL	Arch. Biophys. 120:124-135(1967).
RN	[3]
RP	PARTIAL SEQUENCE (ALLELES C-RHODESIA AND D-ZAMBIA).
RX	MEDLINE=7300789; PubMed=4561255;
RA	Schreeder W.A., Shelton J.R., Shelton J.B., Apell G., Huisman T.H.J., Smith L.L., Carr W.R.,
RT	"Amino acid sequences in the beta-chains of adult bovine hemoglobins C-Rhodesia and D-Zambia";
RA	Arch. Biochem. Biophys. 152:222-232(1972).
RN	[4]
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX	MEDLINE=9401650; PubMed=841160;
RA	Perutz M.F., Poyart C., Pagnier J., Kister J.;
RA	"A novel allosteric mechanism in hemoglobin. Structure of bovine deoxyhemoglobin, absence of specific chloride-binding sites and origin of the chloride-linked Bohr effect in bovine and human haemoglobin. ";
RL	J. Mol. Biol. 233:536-545(1993).
RX	X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RA	MEDLINE=21262557; PubMed=11369847;
RA	Safio M.K., Abraham D.J.;
RT	"The X-ray structure determination of bovine carbonmonoxy hemoglobin at 2.1 Å resolution and its relationship to the quaternary structures of other hemoglobin crystal forms";
RT	Protein Sci. 10:1091-1099(2001);
CC	-1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
RESULT	14
Query	Match
Best Local Similarity	100 %;
Matches	Score 10;
10	DB 1;
Conservative	Length 145;
0;	Pred. No. 4.2e-05;
0;	Mismatches 0;
0;	Indels 0;
0;	Gaps 0;
HBB_ODOVI	STANDARD;
ID	PRT; 145 AA.
AC	P02074;
DT	21-JUL-1986 (Rel. 01, Created)
DT	15-DEC-1998 (Rel. 37, Last annotation update)
DE	Hemoglobin beta-III chain.
GN	Odocoileus virginianus (Virginia white-tailed deer);
OS	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea; Cervidae; Odocoileinae; Odocoileus.
OC	NCBI_TAXID=9875;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=83185439; PubMed=6841126;
RA	Shimizu K., Wong S.C., Wilson J.B., Lam H., Reynolds A.E., Singh P., Huisman T.H.J., Charles N.G., Anna E.L.;
RA	"The primary sequence of the beta chain of Hb type III of the Virginia white-tailed deer (Odocoileus virginianus)", a comparison with putative sequences of the beta chains from four additional deer hemoglobins, types II, IV, V, and VIII, and relationships between

KW	Heme; Oxygen transport; Transport; Erythrocyte.	CC	
FT	METAL 62 62 IRON (HEME DISTAL LIGAND).	CC	
METAL	91 91 IRON (HEME PROXIMAL LIGAND).	CC	
SEQUENCE	145 AA; 16166 MW; 53B625ECA1E1A9 CRG64;	CC	
QY	1 LVVYPWTQRF 10	CC	Query Match 100.0%; Score 10; DB 1; Length 145; Best Local Similarity 100.0%; Pred. No. 4.2e-05; Mismatches 0; Indels 0; Gaps 0;
Db	31 LVVYPWTQRF 40	CC	Best Local Similarity 100.0%; Pred. No. 4.2e-05; Mismatches 0; Indels 0; Gaps 0;
RESULT	17	CC	or send an email to license@isb-sib.ch).
HBB_SHBEP		CC	-----
ID	HBB_SHEP	AC	Heme; Oxygen transport; Transport; Erythrocyte;
STANDARD:		ID	METAL 62 IRON (HEME DISTAL LIGAND).
PRT:	145 AA.	AC	METAL 91 IRON (HEME PROXIMAL LIGAND).
PR02075;	21-JUL-1986 (Rel. 01, Created)	DT	N -> S (IN A ALLELE).
DT	21-JUL-1990 (Rel. 13, Last sequence update)	DR	P -> A (IN A ALLELE).
DT	16-OCT-2001 (Rel. 40, Last annotation update)	DR	MK -> VQ (IN A ALLELE).
DE	Hemoglobin beta chain.	DR	N -> S (IN A ALLELE).
DE	HBB.	DR	D -> E (IN A ALLELE).
OS	Ovis aries (Sheep);	DR	K -> R (IN A ALLELE).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DR	N -> A (IN REF. 4; MAY BE DUE TO A DIFFERENCE IN BREED OF SHEEP).
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	DR	-----
OC	Bovidae; Caprinae; Ovis.	DR	-----
OX	NCBI_TAXID=9940;	DR	-----
RN	[1]	DR	-----
SEQUENCE FROM N.A. (B ALLELE)		DR	-----
RX	MEDLINE=89178744; PubMed=494347;	DR	-----
RA	Gardner K.J.; Lingrel J.B.;	DR	-----
RT	"A comparison of the beta A-and beta B-globin gene clusters of sheep";	DR	-----
RT	J. Mol. Evol. 28:175-184(1989).	DR	-----
RN	[2]	DR	-----
RP	SEQUENCE (B ALLELE).	DR	-----
RX	MEDLINE=67134347; PubMed=6022868;	DR	-----
RA	Boyer S.H.; Hathaway P.; Pascaio F.; Bordley J.; Orton C.,	DR	-----
RA	Naughton M.A.;	DR	-----
RT	"Differences in the amino acid sequences of tryptic peptides from three sheep hemoglobin beta chains.";	DR	-----
RL	J. Biol. Chem. 242:2211-2232(1967).	DR	-----
RN	[3]	DR	-----
RP	SEQUENCE OF 1-29; 39-59; 72-85 AND 104-145 FROM N.A. (A ALLELE).	DR	-----
RX	MEDLINE=81117290; PubMed=6161931;	DR	-----
RA	Kretschmer P.J.; Coon H.C.; Davis A.; Harrison M.; Nienhuis A.W.;	DR	-----
RT	"Hemoglobin switching in sheep. Isolation of the fetal gamma-globin gene and demonstration that the fetal gamma- and adult beta A-globin genes lie within eight kilobase segments of homologous DNA.";	DR	-----
RL	J. Biol. Chem. 256:1975-1982(1981).	DR	-----
RN	[4]	DR	-----
SEQUENCE OF 1-28 FROM N.A. (B ALLELE).		DR	-----
RX	MEDLINE=88216150; PubMed=3367782;	DR	-----
RA	Gardner K.J.; Lingrel J.B.;	DR	-----
RT	"Structural organization of the beta-globin locus of B-haplotype sheep";	DR	-----
RT	Mol. Biol. Evol. 5:134-140(1988).	DR	-----
RN	[5]	DR	-----
RP	VARIANT A ALLELE.	DR	-----
RX	MEDLINE=67209244; PubMed=6033754;	DR	-----
RA	Beale D.;	DR	-----
RT	"A partial amino acid sequence for sheep haemoglobin A.;"	DR	-----
RL	Biochem. J. 103:129-140(1967).	DR	-----
CC	-1 SUBUNIT: HETEROOTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.	DR	-----
CC	-1 TISSUE SPECIFICITY: RED BLOOD CELLS.	DR	-----
CC	-1 POLYMORPHISM: SHEEP HAS TWO ALLELIC BETA CHAINS, A AND B. THE B ALLELE SEQUENCE IS SHOWN.	DR	-----
CC	-1 SIMILARITY: BELONGS TO THE GLOBIN FAMILY.	DR	-----
CC		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RN	[1]	CC	-----
RP	SEQUENCE.	CC	-----
RX	MEDLINE=85279893; PubMed=4026993;	CC	-----
RA	Rodenwald K., Wiesner H., Braunlizer G.;	CC	-----
RT	"Primary structure of the hemoglobins from the greater kudu antelope (tragelaphus strepsiceros)"	CC	-----
RL	Bio. Chem. Hoppe-Seyler 366:395-402(1985).	CC	-----
CC	-1 FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE	CC	-----
CC	-1 VARIOUS PERIPHERAL TISSUES.	CC	-----
CC	-1 SUBUNIT: HETEROOTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.	CC	-----
CC	-1 TISSUE SPECIFICITY: RED BLOOD CELLS.	CC	-----
CC	-1 SIMILARITY: BELONGS TO THE GLOBIN FAMILY.	CC	-----

PIR: A02391; HBOKA.
 DR Heme; Oxygen transport; transport; Erythrocyte;
 DR Polymorphism.
 FT IRON (HEME DISTAL LIGAND).
 METAL IRON (HEME PROXIMAL LIGAND).
 FT VARIANT G -> S (IN A SECOND ALLELE).
 DR PROSITE; PS0103; GLOBIN; 1.
 KW Heme; Oxygen transport; transport; Erythrocyte;
 DR InterPro; IPR002337; Beta-haem.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PR00814; BETAHAEV.
 DR PROSITE; PS0103; GLOBIN; 1.
 KW Heme; Oxygen transport; transport; Erythrocyte.
 FT IRON (HEME DISTAL LIGAND).
 METAL IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 145 AA; 16053 MW; EB05F16E856E7522 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10
 1|||||||
 Db 31 LVVYPTQRF 40

RESULT 19
 HBBL_IGUG STANDARD; PRT; 146 AA.
 ID HBBL_IGUG STANDARD; PRT; 146 AA.
 AC P18987;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Hemoglobin beta-1 chain.
 RN [1]
 RR
 RX MEDLINE=89105321; PubMed=3214555;
 RA Abbas A., Wells R.M.G., Brittain T., Braunitzer G.;
 RT "Primary structure of the hemoglobins from *Sphenodon* (*Sphenodon punctatus*, Tuatara, *Rynchocephalia*). Evidence for the expression of alpha D-gene.";
 RT RT
 RL Biol. Chem. Hoppe-Seyler 369:755-764 (1988).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: THERE ARE THREE FORMS OF HEMOGLOBIN IN SPHENODON: A, A' AND D. HB A IS A TETRAMER OF TWO ALPHA-A AND TWO BETA-1, HB D IS A TETRAMER OF TWO ALPHA-D AND TWO BETA-2.
 CC -1- MISCELLANEOUS: SPHENODON'S HBS HAVE PROPERTIES NOT FOUND IN OTHER REPTILES: POOR COOPERATIVITY, HIGH AFFINITY FOR OXYGEN, SMALL BOHR AND HAEMADYE EFFECTS, APPRECIABLE PHOSPHATE EFFECTS (THOSE PROPERTIES ARE ALSO FOUND IN THE HBS OF PRIMITIVE URODELE AND CACILIAN AMPHIBIANS).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; S0138; HB7J1.
 DR HSSP; P02118; IAAF.
 DR InterPro; IPR002337; Beta-haem.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PR00814; BETAHAEV.
 DR PROSITE; PS0103; GLOBIN; 1.
 KW Heme; Oxygen transport; transport; Erythrocyte.
 FT IRON (HEME DISTAL LIGAND).
 METAL IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 16191 MW; E2714EE2/94081DD CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10
 1|||||||
 Db 32 LVVYPTQRF 41

RESULT 21
 HBBL_TAPTE STANDARD; PRT; 146 AA.
 ID HBBL_TAPTE STANDARD; PRT; 146 AA.
 AC P02064;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta-1 chain (Major).
 DR HBB1.
 OS *Tapirus terrestris* (lowland tapir) (Brazilian tapir).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
 OC NCBI_TaxID=9801;
 RN [1]
 RR
 RX MEDLINE=89053021; PubMed=6149994;
 RA Mazur G., Braunitzer G.;
 RT "Perissodactyla: the primary structure of hemoglobins from the lowland tapir (*Tapirus terrestris*): glutamic acid in position 2 of the beta chains.";

RT RT

RESULT 20
 HBBL_SPHG

RL Hoppe-Seyler's Z. Physiol. Chem. 365:1097-1106(1984).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; A02382; HMPJ.
 DR HSSP; P02062; LIBE.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PRO0814; BETAHAE.
 DR PROSITE; PS01033; GLOBIN_1.
 DR Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15973 MW; 1D53B28D108F6124 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 22
 HBBL_UROHA STANDARD; PRT; 146 AA.
 ID HBBL_UROHA
 AC P18991;
 DT 01-NOV-1990 (Rel. 15, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Hemoglobin beta-1 chain (Fragments),
 Uromastyx hardwickii (Indian spiny-tailed lizard),
 Euteleostomi;
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Uromastycina;
 OC Lepidosauria; Squamata; Iguania; Aetodonta; Agamidae; Uromastycina;
 OC Uromastyx.
 OX NCBI_TaxID=40250;
 [1]
 RP SEQUENCE:
 RX MEDLINE=84029159; PubMed=6628672;
 RA Nagvi S., Zaidi Z.H., von Bahr-Lindstroem H., Carlquist M.,
 RA Joernvall H.;
 RT "Characterization of hemoglobin from the lizard Uromastyx
 hardwickii",
 RLT FEBS Lett. 162:290-295 (1983).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; A05304; A05304.
 DR HSSP; P02112; LIBR.
 DR InterPro; IPR002337; Beta_haem.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PRO0814; BETAHAE.
 DR PROSITE; PS01033; GLOBIN_1.
 DR Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15855 MW; AA82B6EEBE6466BD CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 23
 HBB2_PANLE STANDARD; PRT; 146 AA.
 ID HBB2_PANLE
 AC P18986;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DR 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta-2 chain.
 GN HBB2.
 OS Panthera leo (Lion).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Panthera.
 OX NCBI_TaxID=9689;
 RN [1]
 RP SEQUENCE:
 RA Jahan M., Ahmed A., Braunitzer G., Zaidi Z.H., Goeltenboch R.;
 RT "Carnivora: the primary structures of adult lion (Panthera leo)
 hemoglobins";
 RL Naturforsch. C 42:1465-1470(1987).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; S03926; HBL2.
 DR HSSP; P02023; LABW.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR00971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PROSITE; PS01033; GLOBIN_1.
 DR Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15855 MW; AA82B6EEBE6466BD CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 24
 HBB2_TAPTE STANDARD; PRT; 146 AA.
 ID HBB2_TAPTE
 AC P02065;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta-2 chain (Minor).
 GN HBB2.
 OS Tapirus terrestris (Lowland tapir) (Brazilian tapir).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
 OX NCBI_TaxID=9801;
 RN [1]
 RP SEQUENCE:
 RX MEDLINE=85053021; PubMed=6149994;
 RA Mazur G., Braunitzer G.;
 RT "Perissodactyla: the primary structure of hemoglobins from the
 lowland tapir (Tapirus terrestris): glutamic acid in position 2 of
 the beta chains";
 RL Hoppe-Seyler's Z. Physiol. Chem. 365:1097-1106(1984).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

-!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

CC DR PIR: A0283; HBTNP.

DR HSSP; P02062; LIBE.

DR InterPro; IPR002337; Beta_haem.

DR InterPro; IPR000971; Globin.

DR Pfam; PF00042; globin_1.

DR PRINTS; PR00814; BETAHAEAM.

DR PROSITE; PS01033; GLOBIN_1.

KW Heme; Oxygen transport; Transport; Erythrocyte.

FT METAL 63 63 IRON (HEME DISTAL LIGAND).

FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).

SQ SEQUENCE 146 AA; 16004 MW; D48E0271F554271 CRC64;

RESULT 25

HBB_AILFU STANDARD; PRT; 146 AA.

AC ID HBB_AILME STANDARD; PRT; 146 AA.

ID HBB_AILFU STANDARD; PRT; 146 AA.

AC AC P18533;

DT DT 01-Nov-1990 (Rel. 16, Created)

DT DT 01-Nov-1990 (Rel. 16, Last sequence update)

DT DT 16-Oct-2001 (Rel. 40, Last annotation update)

DE DE Hemoglobin beta chain.

GN GN Alluropoda melanoleuca (Giant Panda).

OS OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Alluropoda.

OX OX NCBI_TaxID=9646;

RN RN [1]

RP RP SEQUENCE.

RX RX MEDLINE=87014854; PubMed=3762727;

RA RA Tagle D.A., Miyamoto M.M., Goodman M., Hofmann O., Braunitzer G.,

RA Goettltenboch R., Jalanka H.,

RT RT "Hemoglobin of pandas: phylogenetic relationships of carnivores as ascertained with protein sequence data.";

RL RL Naturwissenschaften 73:512-514 (1986).

CC CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.

CC CC -!- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR DR PIR: S0529; HRFGQ.

DR DR HSSP; P0203; IBAB.

DR DR InterPro; IPR002337; Beta_haem.

DR DR Pfam; PF00042; globin_1.

DR DR PRINTS; PR00814; BETAHAEAM.

KW KW PROSITE; PS01033; GLOBIN_1.

OS OS Heme; Oxygen transport; Transport; Erythrocyte.

OC OC METAL 63 63 IRON (HEME DISTAL LIGAND).

FT FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).

SQ SQ SEQUENCE 146 AA; 16021 MW; 756DD35108E67EA2 CRC64;

RESULT 25

HBB_AILFU STANDARD; PRT; 146 AA.

AC AC P18533;

DT DT 01-Nov-1990 (Rel. 16, Created)

DT DT 01-Nov-1990 (Rel. 16, Last sequence update)

DT DT 16-Oct-2001 (Rel. 40, Last annotation update)

DE DE Hemoglobin beta chain.

GN GN Alluropoda melanoleuca (Giant Panda).

OS OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Alluropoda.

OX OX NCBI_TaxID=9646;

RN RN [1]

RP RP SEQUENCE.

RX RX MEDLINE=37014854; PubMed=3762727;

RA RA Tagle D.A., Miyamoto M.M., Goodman M., Hofmann O., Braunitzer G.,

RA Goettltenboch R., Jalanka H.,

RT RT "Hemoglobin of pandas: phylogenetic relationships of carnivores as ascertained with protein sequence data.";

RL RL Naturwissenschaften 73:512-514 (1986).

CC CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.

CC CC -!- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR DR PIR: S0529; HRFGQ.

DR DR HSSP; P0203; IBAB.

DR DR InterPro; IPR002337; Beta_haem.

DR DR Pfam; PF00042; globin_1.

DR DR PRINTS; PR00814; BETAHAEAM.

KW KW PROSITE; PS01033; GLOBIN_1.

OS OS Heme; Oxygen transport; Transport; Erythrocyte.

OC OC METAL 63 63 IRON (HEME DISTAL LIGAND).

FT FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).

SQ SQ SEQUENCE 146 AA; 15950 MW; B2082BB94463B2BB CRC64;

RESULT 27

HBB_ANTPA STANDARD; PRT; 146 AA.

AC AC P14338;

DT DT 01-Jan-1990 (Rel. 13, Created)

DT DT 01-Jan-1990 (Rel. 13, Last sequence update)

DT DT 16-Oct-2001 (Rel. 40, Last annotation update)

DE DE Hemoglobin beta chain.

GN GN HBB.

OS OS Antrozous pallidus (Pallid bat).

OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Vespertilionidae;

OC OC Antrozous;

OX OX NCBI_TaxID=9440;

RN RN [1]

RP RP SEQUENCE.

RX RX MEDLINE=88050104; PubMed=3675871;

RA RA Kleinischmidt T., Koop B.F., Braunitzer G.,

RT RT "The primary structure of the pallid bat (Antrozous pallidus) hemoglobin.";

RT RT Chirptera) hemoglobin.

RL RL Biol. Chem. Hoppe-Seyler 368:1197-1202(1987).

CC CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.

CC CC -!- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR DR PIR: B229702; B229702.

RESULT 26

HBB_AILME

DR	HSSP; P02023; BAB.	DT	21-JUL-1986 (Rel. 01. Created)
DR	InterPro; IPR02337; Beta-haem.	DT	22-NOV-1990 (Rel. 01. Last sequence update)
ID	IPR000971; Globin.	DT	16-OCT-2001 (Rel. 40. Last annotation update)
Pfam	Pfam; PF00042; globin_1.	DE	Hemoglobin beta chain.
PRINTS	PRINTS; PRO0814; BETAHAEM.	GN	HBB.
DR	PROSITE; PS01033; BEPAHAE.	OS	Atelos geoffroyi (Black-handed spider monkey), Atelos paniscus (Black spider monkey), and Atelos belzebuth (Long-haired spider monkey).
KW	Heme; Oxygen transport; Transport; Erythrocyte.	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metazoa; Craniata; Vertebrata; Atelinae; Atelos.
FT	METAL; 63 63 IRON (HEME DISTAL LIGAND).	OC	NCBI_TaxID=9509, 9510, 9507;
FT	METAL; 92 92 IRON (HEME PROXIMAL LIGAND).	OC	[1]
SQ	SEQUENCE	RN	SEQUENCE.
RESULT	28	RN	RC SPECIES=A. geoffroyi, and A.belzebuth;
HBB_AOTTR		RP	RX MEDLINE=7202019; PubMed=499925;
ID	HBB_AOTTR	RC	RX MEDLINE=70031568; PubMed=4981734;
AC	P020235;	RA	RA Boyer S.H., Crosby E.F., Noyes A.N., Fuller G.F., Leslie S.E., Adams J.G.;
DT	21-JUL-1986 (Rel. 01. Created)	RT	RT "The structure and biosynthesis of hemoglobins A and A2 in the new world Primate Atelos paniscus: a preliminary account.";
DT	21-JUL-1986 (Rel. 01. Last sequence update)	RL	RL Ann. N.Y. Acad. Sci. 165:360-377 (1969).
DT	16-OCT-2001 (Rel. 40. Last annotation update)	CC	CC "Primate hemoglobins: Some sequences and some proposals concerning the character of evolution and mutation.";
DE	Hemoglobin beta chain.	CC	CC - - SUBUNIT: HEMEROPETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
HBB		CC	CC - - TISSUE SPECIFICITY: RED BLOOD CELLS.
ATOTUS	ATOTUS trivirgatus (Night monkey) (Douroucouli).	CC	CC - - SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DR	DR PIR; A02355; HBWKH.
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Atotus.	DR	DR PIR; A90034; HBMKK.
NCBI_TaxID=9505;		DR	DR HSSP; P02023; IBAB.
[1]	SEQUENCE.	DR	DR InterPro; IPR02337; Beta-haem.
RX	MEDLINE=72020149; PubMed=4999925;	DR	DR InterPro; IPR000971; Globin.
RA	Boydson S.H., Crosby E.F., Noyes A.N., Fuller G.F., Leslie S.E.,	DR	DR Pfam; PF00042; globin_1.
RT	"Primate hemoglobins: Some sequences and some proposals concerning the character of evolution and mutation.";	DR	DR PRINTS; PRO0814; BETAHAEM.
RT	Bioclin. Genet. 5:405-448(1971).	DR	DR PROSITE; PS01033; GLOBIN_1.
RL	- - FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.	KW	KW Heme; Oxygen transport; Transport; Erythrocyte.
CC	- - SUBUNIT: HEMEROPETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.	FT	FT METAL; 63 63 IRON (HEME DISTAL LIGAND).
CC	- - TISSUE SPECIFICITY: RED BLOOD CELLS.	FT	FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
CC	- - SIMILARITY: BELONGS TO THE GLOBIN FAMILY.	SQ	SQ SEQUENCE 146 AA; 15913 MW; EDB309B8A214B095 CRC64;
PIR	PIR; A02356; HBWKH.		
DR	HSSP; P02023; IBAB.		
DR	InterPro; IPR02337; Beta-haem.		
DR	InterPro; IPR000971; Globin.		
DR	Pfam; PF00042; globin_1.		
DR	PRINTS; PRO0814; BETAHAEM.		
DR	PROSITE; PS01033; GLOBIN_1.		
KW	Heme; Oxygen transport; Transport; Erythrocyte.		
FT	METAL; 63 63 IRON (HEME DISTAL LIGAND).		
FT	METAL; 92 92 IRON (HEME PROXIMAL LIGAND).		
SQ	SEQUENCE 146 AA; 15913 MW; EDB309B8A214B095 CRC64;		
RESULT	30		
HBB_BALAC			
ID	HBB_BALAC	STANDARD	146 AA.
AC	P18984;		
DT	01-NOV-1990 (Rel. 16. Created)		
DT	01-NOV-1990 (Rel. 16. Last sequence update)		
DT	16-OCT-2001 (Rel. 40. Last annotation update)		
DE	Hemoglobin beta chain.		
GN			
OS	Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Cetaceae; Mysticeti;		
OC	Balaenopteridae; Balaenoptera.		
OX	NCBI_TaxID=9767;		
RN	[1]		
RP	SEQUENCE.		
Query	Match	100.0%	Score 10; DB 1; Length 146;
Best Local Similarity	100.0%	Pred. No. 4.2e-05;	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches	10;		
OY	1	LVVPYPTWQRF 10	
QY	1	LVVYPTWQRF 10	
Db	32	LVVYPTWQRF 41	
RESULT	29		
HBB_ATEGE			
ID	HBB_ATEGE	STANDARD	146 AA.
AC	P02024;		
RP	SEQUENCE.		

RX MEDLINE=72076589; PubMed=5002362;
 RA Nutt P.E., Sullivan B.;
 RT "Primate hemoglobins: their structure, function and evolution. I.
 Amino acid compositions of the tryptic peptides from the beta chain
 of *Cebus albifrons*";
 RL Comp. Biochem. Physiol. 39B:797-814 (1971).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 -!- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02361; HMQA.
 DR HSSP; P02023; IDXT.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15989 MW; 5B88ED3BA6020DC CRC64;

Query Match 100 %; Score 10; DB 1; Length 146;
 Best Local Similarity 100 %; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 VARIANT 13 13 0; 0; 0; 0;

QY 1 LVVYPWTQRF 10
 |||||||||
 Db 32 LVVYPWTQRF 41

RESULT 34

HBB_CEBAP STANDARD; PRT; 146 AA.

ID HBB_CEBAP STANDARD; PRT; 146 AA.

AC P02041;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OC Cercopithecus aethiops (Green monkey) (Griver).
 OC Eukaryota; Metazoa; Chorata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75040050; PubMed=4214754;
 RA Matsuda G., Maita T., Watanabe B., Araya A., Morokuma K., Goodman M.,
 RA Pychiodko W.;
 RT "The amino acid sequences of the alpha and beta polypeptide chains of
 adult hemoglobin of the savannah monkey (*Cercopithecus aethiops*)";
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1153-1155(1973).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: B02252; HBKG.
 DR HSSP; P02023; IBAB.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15927 MW; OFCD16DA69209CDE CRC64;

Query Match 100 %; Score 10; DB 1; Length 146;
 Best Local Similarity 100 %; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||||||
 Db 32 LVVYPWTQRF 41

RESULT 36

HBB_CERSI STANDARD; PRT; 146 AA.

ID HBB_CERSI STANDARD; PRT; 146 AA.

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 HBB.
 GN Ceratotherium simum (white rhinoceros) (square-lipped rhinoceros).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
 OX NCBI_TAXID=9807;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=63055102; PUBMED=7141412;
 RA Mazur G.; Braunitzer G.; Wright P.G.;
 RT "The primary structure of the hemoglobin from a white rhinoceros
 (Ceratotherium simum, perissodactyla); beta 2 Glu";
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1077-1085(1982).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 CC -1- MISCELLANEOUS: THE VARIANTS FOUND IN THIS SAMPLE FROM A SINGLE
 CC ANIMAL SUGGEST THE PRESENCE OF AT LEAST TWO BETA CHAIN LOCI.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A04621; HEMKB.
 DR HSSP: P02023; IBAB.
 DR InterPro: IPRO02337; Beta_haem.
 DR Pfam: PF00042; globin; 1.
 DR PRINS: PR00814; BETAHABM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; oxygen transport; transport; erythrocyte.
 FT METAL 63 63 IRON (HEME PROXIMAL LIGAND).
 FT METAL 92 92 IRON (HEME DISTAL LIGAND).
 SQ SEQUENCE 146 AA; 15995 MW; QADE3525EDC6BB5 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 ID HBB_COLBA
 AC P02033;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 HBB
 OS Colobus badius (Red colobus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
 OC Colobus.
 OX NCBI_TAXID=9571;
 RN [1]
 RP SEQUENCE.
 RA Hewett-Emmett D.; Barnicot N.A.;
 RL Unpublished results, cited by:
 RL Yasunobu K.T.; Tanaka M.;
 RL (In) Fashan G.D. (eds.);
 RL Handbook of biochemistry and molecular biology (3rd ed.),
 RL pp. 3:441-460, CRC Press, Cleveland (1976).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: B04620; HMBQB.
 DR HSSP: P02023; IBAB.
 DR InterPro: IPRO02337; Beta_haem.
 DR Pfam: PF00042; globin; 1.
 DR PRINS: PR00814; BETAHABM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; oxygen transport; transport; erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15870 MW; 314B60C810F76C9A CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 ID HBB_COLBA
 AC P02033;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 HBB
 OS Cercopithecus torquatus atys (red-crowned mangabey) (sooty mangabey).
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Buxtorf, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TAXID=9331;
 RN [1]
 RP SEQUENCE.
 RA Cook C.N.; Barnicot N.A.;
 RL Unpublished results, cited by:
 RL Yasunobu K.T.; Tanaka M.;
 RL (In) Fashan G.D. (eds.);
 RL Handbook of biochemistry and molecular biology (3rd ed.),
 RL pp. 3:441-460, CRC Press, Cleveland (1976).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.

RESULT 39
 HBB_COLPO STANDARD; PRT; 146 AA.
 ID HBB_COLPO STANDARD; PRT; 146 AA.
 AC P19815;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Colobus polykomos.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
 OC Colobus.
 OC Colobus.
 RN NCBI_TaxID=9572;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9342433; PubMed=2760921;
 RA Vincent K.A., Wilson A.C.;
 RT "Evolution and transcription of old world monkey globin genes.";
 RL J. Mol. Biol. 207:65-48(1989).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROOTRIMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

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CC EMBL; J00330; -!- NOT_ANNOTATED_CDS.
 DR PIR; S04615; S04615.
 DR HSSP; P02023; IBAB.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT INIT_MET 0 IRON (HEME DISTAL LIGAND).
 FT METAL 63 63 IRON (HEME PROXIMAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 16017 MW; FC1994B66F07CC34 CRC64;

RESULT 41
 HBB_CTFEGU STANDARD; PRT; 146 AA.
 ID HBB_CTFEGU STANDARD; PRT; 146 AA.
 AC P20855;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 OS Ctenodactylus gundi (Northern gundi).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Ctenodactyliidae;
 OC Ctenodactylus.
 RN NCBI_TaxID=10166;
 [1]
 RP SEQUENCE.
 RX MEDLINE=91197427; PubMed=2085415;
 RA Beintema J.J., Rodewald K., Braunitzer G.;
 RT "The primary structures of gundi (Ctenodactylus gundi, Rodentia) hemoglobin and myoglobin";
 RL Biol. Chem. Hoppe-Seyler 371:089-099(1990).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROOTRIMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PTR; S13283; HBTNG.
 DR HSSP; P02067; IQFW.
 DR InterPro; IPR00337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15846 MW; F3D582E665E182F8 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;

Query Match Best Local Similarity 100.0%; Pred. No. 4.2e-05; Indels 0; Gaps 0; Mismatches 10; Conservative 0;

Qy 1 LVVYPTWQRF 10
 Db 32 LVVYPTWQRF 41

RESULT 40
 HBB_CROCR STANDARD; PRT; 146 AA.
 ID HBB_CROCR STANDARD; PRT; 146 AA.
 AC P18986;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Crocetta crocetta (Spotted hyena).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Hyaenidae; Crocetta.
 OC NCBI_TaxID=9678;
 RN [1]

SQ SEQUENCE 146 AA; 16134 MW; 43FFAED7AD7EBC9D CRC64;

Query Match Best Local Similarity 100.0%; Score 10; DB 1; Length 146; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 45

HBB_EQUH EQUH STANDARD; PRT; 146 AA.

ID HBB_EQUH
AC P02063;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.

CC Equus hemionus kulan (Kulan) (Asiatic wild ass), and
Equus zebra (Mountain zebra); Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TAXID=73334; 9791;

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TAXID=73334; 9791;

RP SEQUENCE:[1]
RX MEDLINE=82140509; PubMed=7061044;
RN [1]
RA Mazur, G.; Braunitzer, G.;
RT "The sequence of hemoglobins from an asiatic wild ass and a mountain zebra. ";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:59-71(1982);
CC InterPro: IPR02337; Beta-haem.
CC - FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
CC - SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC - TISSUE SPECIFICITY: RED BLOOD CELLS.
CC - SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR PIR: A02381; HBOZ;
DR PIR: A91705; HBOC.
DR HSSP; P02062; LIBE.
DR InterPro: IPR002337; Beta-haem.
DR InterPro: IPR000971; Globin.
DR Pfam; PF00042; globin_1.
DR PROSITE; PS01033; GLOBIN_1.
DR Heme; Oxygen transport; transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
FT SEQUENCE 146 AA; 15805 MW; 0E1520B80808D82B CRC64;

OX NCBI_TAXID=40322;

Query Match Best Local Similarity 100.0%; Score 10; DB 1; Length 146; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 47

HBB_EULFU EULFU STANDARD; PRT; 146 AA.

ID HBB_EULFU
AC P02053;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.

GN HBB.

OS Eulemur fulvus fulvus (Brown lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Strepsirrhini; Lemuridae; Eulemur.
OX NCBI_TAXID=40322;

RN [1]
RP SEQUENCE.

RX MEDLINE=79150872; PubMed=107155;
RA Maita, T., Setoguchi, M., Matsuda, G., Goodman, M.,
RT "Amino acid sequences of the alpha and beta chains of adult hemoglobin of the brown lemur, Lemur fulvus fulvus.",
J. Biochem. 85:755-764(1979).

RN [2]
RP SEQUENCE FROM N. A.
RX MEDLINE=88174365; PubMed=3444413;
RA Harris, S., Thackeray, J. R., Jeffrey, A. J., Weiss, M. L.;
RT "Nucleotide sequence analysis of the lemur beta-globin gene family: evidence for major rate fluctuations in globin polypeptide evolution.",
RT evolution.",
RL Mol. Biol. Evol. 3:455-484(1986).
CC - FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
CC - SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC - TISSUE SPECIFICITY: RED BLOOD CELLS.
CC - SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

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OX NCBI_TAXID=9365;
RN [1]
RP SEQUENCE.
RX MEDLINE=79109529; PubMed=762046;
RA Maita, T., Araya, A., Matsuda, G., Goodman, M.;
RT "Amino acid sequences of the alpha and beta chains of adult hemoglobin of the European hedgehog, Erinaceus europaeus.",
J. Biochem. 85:259-269(1979).
CC - FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
CC - SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC - TISSUE SPECIFICITY: RED BLOOD CELLS.
CC - SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: A02377; HBOH.
DR HSSP; P02067; 10PW.
DR InterPro; IPR02337; Beta-haem.
DR InterPro: IPR00971; Globin.
DR Pfam; PF00042; globin_1.
DR PRINTS; PS01033; GLOBIN_1.
DR PROSITE; PS01033; GLOBIN_1.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
FT SEQUENCE 146 AA; 15805 MW; 0E1520B80808D82B CRC64;

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 CC or send an email to license@isb-sib.ch.)

DR EMBL; M15734; AAA36822.1; -.

DR PIR; A02370; RBLEF.

DR HSSP; P00233; 2HHE.

DR InterPro; IPR002337; Beta_haem.

DR InterPro; IPR000971; Globin.

DR Pfam; PR00042; globin; 1.

DR PRINTS; PR00814; BETAHAEAM.

DR PROSITE; PS01033; GLOBIN; 1.

KW Heme; Oxygen transport; Transport; Erythrocyte.

FT INIT_MET 0

FT METAL 63 63 IRON (HEME DISTAL LIGAND).

FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).

FT SEQUENCE 146 AA; 15770 MW; 2D08B507/D6FCED CRC64;

SQ OS Gorilla gorilla gorilla (Lowland gorilla).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OS Euarchontoglires; Mammalia; Eutheria; Primates; Strepsirrhini; Galagonidae; Otolemur.

Db 32 LVVYPWTQRF 41

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Deletions 0; Insertions 0;

Qy 1 LVVYPWTQRF 10

||| ||| |||

Db 32 LVVYPWTQRF 41

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Deletions 0; Insertions 0;

Qy 1 LVVYPWTQRF 10

||| ||| |||

Db 32 LVVYPWTQRF 41

RESULT 48

HBB_FELCA STANDARD; PRT; 146 AA.

ID HBB_FELCA

AC P07412;

DT 01-APR-1988 (Rel. 07, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DE Hemoglobin beta-A and beta-B chains.

GN FELIS

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI_TAXID=9685;

RN [1]

RP MEDLINE-861050915; PubMed=4063071;

RA Abbasi A.; Braunitzer G.;

RT "The primary structure of hemoglobins from the domestic cat (Felis catus, Felidae).";

RL Biol. Chem. Hoppe-Seyler 366:699-704(1985).

CC -- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.

CC -- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC -- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC -- POLYMORPHISM: THERE ARE TWO ALLELES. THE SEQUENCE SHOWN IS THAT OF BETA-1.

CC -- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR PIR; A02367; HBGC.

DR HSSP; P02023; 1BAB.

DR InterPro; IPR002337; Beta_haem.

DR InterPro; IPR000971; Globin.

DR Pfam; PR00042; globin; 1.

DR PRINTS; PR00814; BETAHAEAM.

DR PROSITE; PS01033; GLOBIN; 1.

KW Heme; Oxygen transport; Transport; Erythrocyte;

FT POLYMORPHISM.

FT METAL 63 63 IRON (HEME DISTAL LIGAND).

FT VARIANT 125 125 E -> Q (IN BETA-2).

FT SEQUENCE 146 AA; 15934 MW; FC2BEB1E091FACEE CRC64;

SQ OS Gorilla gorilla gorilla (Lowland gorilla).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OS Euarchontoglires; Mammalia; Eutheria; Primates; Strepsirrhini; Galagonidae; Otolemur.

Db 32 LVVYPWTQRF 41

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Deletions 0; Insertions 0;

Qy 1 LVVYPWTQRF 10

||| ||| |||

Db 32 LVVYPWTQRF 41

RESULT 50

HBB_GORGO STANDARD; PRT; 146 AA.

ID HBB_GORGO

AC P02024;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.

GN HBB

OS Gorilla gorilla gorilla (Lowland gorilla).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 OC NCBI_TaxID=9595;
 OX [1]
 RP SEQUENCE.
 RA Zuckerkandl E.;
 RL Submitted (JUL-1966) to the PIR data bank.
 RN [2]
 RP SEQUENCE OF 1-120 FROM N.A.
 RX MEDLINE=92211718; PUBMED=1556740;
 RA Perrin-Pecoulal P., Gouy M., Nigon V.M., Trabuchet G.;
 RT "Evolution of the primate beta-globin gene region: nucleotide
 sequence of the delta-beta-globin intergenic region of gorilla and
 phylogenetic relationships between African apes and man.";
 J. Mol. Evol. 34:17-30(1992).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X61109; CAA41421.1; -.
 DR PIR; S24304; HGSC.
 DR HSSP; P02023, 1BAB.
 DR Interpro; IPR002337; Beta_haem.
 DR Pfam; PF00027; globin_1.
 DR PRINS; PRO0814; BEPAHAE.
 DR PRINS; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT INIT_MET 0
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 FT SEQUENCE 146 AA; 15839 MW; EACBD9C8F33966A1 CRC64;

RESULT 52
 HBB_HIPAM STANDARD; PRT; 146 AA.
 ID P19016;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 15, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RA Matsuda G., Maita T., Braunitzer G., Schrank B.;
 RT "Hemoglobins, XXXIII. Note on the sequence of the hemoglobins of the
 horse.", Hoppe-Seyler's Z. Physiol. Chem. 361:1107-1116(1980).
 RP SEQUENCE.
 RX MEDLINE=81005583; PubMed=7409745;
 RX MEDLINE=68397920; PubMed=4876811;
 RA Smith D.B.;
 RT "Amino acid sequences of some tryptic peptides from the beta-chain of
 horse hemoglobin.", Can. J. Biochem. 46:825-843(1968).
 RN [3]
 RP DETERMINATION OF AMIDES, AND SEQUENCE OF 52-54.
 RX MEDLINE=71027939; PubMed=5529382;
 RA Smith D.B., Chung W.P.;
 RT "Amide groups of some tryptic peptides from the beta-chain of horse
 hemoglobin.", Can. J. Biochem. 48:1160-1164(1970).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=78007980; PubMed=561852;
 RA Ladner R.C., Heidner E.J., Peritz M.F.;
 RT "The structure of horse methaemoglobin at 2.0-A resolution.",
 J. Mol. Biol. 114:385-414(1977).
 RL PIR; A02380; HBPO.
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR HSSP; P02070; 1HDA.
 DR Interpro; IPR002337; Beta_haem.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PR00814; BEPAHAE.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 16065 MW; 70315747FBED6FEE6 CRC64;

Query Match 100 %; Score 10; DB 1; Length 146;
 Best Local Similarity 100 %; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00014; globin_1.
 DR PRINTS; PRO00814; BETAHBEM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; transport; Erythrocyte;
 3D-structure.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 FT HELIX 5 15
 FT TURN 16 17
 FT HELIX 20 34
 FT HELIX 36 45
 FT HELIX 51 55
 FT TURN 56 56
 FT HELIX 58 75
 FT TURN 76 77
 FT HELIX 78 84
 FT HELIX 86 93
 FT TURN 94 95
 FT HELIX 101 121
 FT HELIX 124 142
 SEQUENCE 146 AA; 16008 MW; 734664793DA642BE CRC64;
 Query Match 100 %; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LVVYPQTQRF 10
 Db 32 LVVYPQTQRF 41
 RESULT 53
 HBB_HUMAN STANDARD; PRT; 146 AA.
 AC P02033; Q14510; Q14481; Q13852; Q9UCP8; Q9UC9;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Homo sapiens (Human),
 OS Pan troglodytes (Chimpanzee), and
 OS Pan paniscus (Pygmy Chimpanzee) (Bonobo).
 OC Eukaryota; Metazoa; Chorlara; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoide; Homo.
 OC NCBI-TAXID=9606; 9598; 9597;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Human;
 RC BRAUNSTEIN; Gehring-Muller R., Hilschmann N., Hilse K., Hobom G.,
 RA Rudloff V., Wittmann-Liebold B.;
 RT "the constitution of normal adult human haemoglobin.";
 RN Hoppe-Seyler's Z. Physiol. Chem. 325:283-286(1961).
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=81054657; PubMed=6254664;
 RA "The nucleotide sequence of the human beta-globin gene.";
 RL Cell 21:647-651(1980).
 RN [3]
 SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=7712643; PubMed=010344;
 RA Marotta C., Forget B., Cohen-Solal M., Weissman S.M.;
 RT "Nucleotide sequence analysis of coding and noncoding regions of human
 beta-globin mRNA.";
 RT Prog. Nucleic Acid Res. Mol. Biol. 19:165-175(1976).
 RN [4]

RP SEQUENCE FROM N.A.
 RA LU L.-, Hu Z.H.-, Du C.S.-, Fu Y.S.-,
 RT "DNA sequence of the human beta-globin gene isolated from a healthy
 Chinese.";
 RT Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
 RN [15]
 SEQUENCE FROM N.A., AND VARIANT DURRRAM-N.C.
 RP
 RC TISSUE=Blood;
 RA Kutlar F., Abdou M., Leithner C., Holley L., Brisco J., Kutlar A.;
 RT "Electrophoretically silent, very unstable, thalassemic mutation at
 codon 114 of beta globin (hemoglobin Durham-N.C.) detected by cDNA
 sequencing of mRNA, from a Russian woman.";
 RT Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 RL [16]
 SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Skeletal muscle;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 RN [17]
 RP SEQUENCE FROM N.A., AND VARIANT LOUISVILLE.
 RC TISSUE=Blood;
 RA Kutlar F., Harbin J., Brisco J., Kutlar A.;
 RT "Rapid detection of electrophoretically silent, unstable human
 hemoglobin 'Louisville', (Beta; Phe 42 Leu/PTT to CTT) by cDNA
 sequencing of mRNA.";
 RT Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 RL [18]
 RP SEQUENCE OF 121-146 FROM N.A.
 RC SPECIES=Human;
 RA MEDLINE=8520533; PubMed=2581851;
 RA Lang K.M., Spritz R.A.;
 RT "Cloning, specific complete polyadenylated 3'-terminal cDNA
 RT segments.";
 RL [19]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF DEOXYHEMOGLOBIN.
 RC SPECIES=Human;
 RX MEDLINE=76027820; PubMed=117732;
 RA Fermi G.;
 RT "Three-dimensional fourier synthesis of human deoxyhaemoglobin at
 RT 2.5-A resolution: refinement of the atomic model.";
 RL J. Mol. Biol. 97:237-256(1975).
 RN [10]
 RP SEQUENCE.
 RC SPECIES=P. troglodytes;
 RX MEDLINE=66071196; PubMed=5855051;
 RA Rifkin D.B., Konigberg W.;
 RT "The characterization of the tryptic peptides from the hemoglobin of
 RT the chimpanzee (Pan troglodytes).";
 RL Biochim. Biophys. Acta 104:457-461(1965).
 RN [11]
 RP SEQUENCE.
 RC SPECIES=P. paniscus;
 RX MEDLINE=83192965; PubMed=6406908;
 RA Goodman M., Braunitzer G., Stangl A., Schrank B.;
 RT "Evidence on human origins from haemoglobins of African apes.";
 RL Nature 303:546-548(1983).
 RN [12]
 RP HAPTOGLOBIN-BINDING.
 RC SPECIES=Human;
 RX MEDLINE=8242088; PubMed=3718478;
 RA Yoshioka N., Attassi M.Z.;
 RT "Haemoglobin binding with haptoglobin. Localization of the
 RT haptoglobin-binding sites on the beta-chain of human haemoglobin by
 RT synthetic overlapping peptides encompassing the entire chain.";
 RL Biochem. J. 234:453-456(1986).
 RN [13]
 RP GLYCATION IN N-TERMINUS.
 RC SPECIES=Human;
 RX MEDLINE=78138998; PubMed=635569;
 RA Dunn H.F., Gabay K.H., Gallop P.M.;
 RT "The glycosylation of hemoglobin: relevance to diabetes mellitus.";
 RL Science 200:21-27(1978).

[14] RN
RN RP VARIANT ALABAMA;
RX MEDLINE=5109326; PubMed=1115799;
RN RA Brimhall B., Jones R.T., Schneider R.G., Hosty T.S., Tomlin G.,
RA Atkins R.;
RT "Two new hemoglobins. Hemoglobin Alabama (beta₁a39(C5)Gln leads to Lys
and hemoglobin Montgomery (alpha₁(CD 6) Leu leads to Arg).";
RL Blochim. Biophys. Acta 379:28-32(1975).
RN [15]
RP VARIANT ALESHA.
RX MEDLINE=93322192; PubMed=8330974;
RA Molchanova T.P., Postnikov Y.V., Pobedimskaya D.D., Smetanina N.S.,
RA Moschan A.A., Kazanetz E.G., Tokarev I.N., Huisman T.H.J.;
RT "Hb Alesha or alpha₂ beta₂ beta₂ (2167(E11)Vai-->Met: a new unstable
hemoglobin variant identified through sequencing of amplified DNA.;"
RL Hemoglobin 17:217-225(1993).
RN [16]
RP VARIANT J-ALTGEIDS GARDENS.
RX MEDLINE=73067354; PubMed=721609;
RA Adams J.G. III, Przywara K.P., Heller P., Shamsudin M.;
RT "Hemoglobin J Altgieds Gardens. A hemoglobin variant with a
substitution of the proximal histidine of the beta-chain.;"
RL Hemoglobin 2:403-415(1978).
RN [17]
RP VARIANT J-ANKARAS.
RX MEDLINE=4297198; PubMed=4850241;
RA Arcasoy A., R., Leumann H., Cavidar A.O., Berki A.;
RT "A new haemoglobin J from Turkey -- Hb Ankara (beta₁₀(A7) Ala-Asp).";
RL FEBS Lett. 42:121-123(1974).
RN [18]
RP VARIANT J-ANKARAS AND COMPLUTENSE.
RX MEDLINE=802116227; PubMed=3707969;
RA Huisman T.H.J., Wilson J.B., Kutlar A., Yang K.-G., Chen S.-S.,
Webber B.B., Altay C., Martinez A.V.;
RT "Hb J-Ankarya or alpha₂ beta₂ (2)5(E9)Lys-->Met. in a Turkish family
and Hb Complutense or alpha₂ beta₂ (2)7(H5)Gln-->Glu in a Spanish
family; correction of a previously published identification.;"
RL Biochim. Biophys. Acta 871:229-231(1986).
RN [19]
RP VARIANT J-AUCKLAND.
RX MEDLINE=80006903; PubMed=3655265;
RA Williamson D., Wells R.M.G., Anderson R., Matthews J.;
RT "A new unstable and low oxygen affinity hemoglobin variant: Hb J-
Auckland [beta₂ 25(B')GLY-->Asp].";
RL [20]
RP VARIANT AUTORA.
RX MEDLINE=96352910; PubMed=8718692;
RA Lafferty J., Ali M., Matthew K., Eng B., Patterson M., Waye J.S.;
RT "Identification of a new high oxygen affinity hemoglobin variant: Hb
Autora [beta₁ 139(H17) Asp-->Tyr].";
RL Hemoglobin 19:335-341(1995).
RN [21]
RP VARIANT B-EST.
RX MEDLINE=80256755; PubMed=3384710;
RA Baudin-Chich V., Wajcman H., Gombaud-Saintonge G., Arous N., Riou J.,
RA Briere J., Galactéros F.;
RT "Hemoglobin B-est [beta₁ 127(H5)Gin-->Lys] a new unstable human
hemoglobin variant located at the alpha₁ beta₁ interface with
specific electrophoretic behavior.;"
RL Hemoglobin 12:179-188(1988).
RN [22]
RP VARIANT BRISBANE.
RX MEDLINE=8129159; PubMed=6165590;
RA Brennen S.O., Wells R.M., Smith H., Carrrell R.W.;
RT "Hemoglobin Brisbane [beta₁ 68 Leu replaced by His. A new high oxygen
affinity variant.;"
RL Hemoglobin 5:325-335(1981).
RN [23]
RP VARIANT BUNBURY.
RX MEDLINE=84031649; PubMed=6629823;
RA Como P.F., Bennett D., Wilkinson T., Kronenberg H.;
RT "A new hemoglobin with high oxygen affinity -- hemoglobin Bunbury:
[14]

RT alpha 2 beta 2 [94 (FG1) Asp replaced by Asn].";
RL Hemoglobin 7:413-421(1983).
RN [24]
RP VARIANT J-CAIRO.
RX MEDLINE=76114933; PubMed=1247583;
RA Garel M.-C., Hassan W., Coquelet M.T., Goossens M., Rosa J., Arouca N.;
RT "Hemoglobin J Cairo: beta 65 (E9) Lys leads to Glu, A new hemoglobin
variant discovered in an Egyptian family.;"
RL Blochim. Biophys. Acta 420:97-104(1976).
RN [25]
RP VARIANT CAMPERDOWN.
RX MEDLINE=75184109; PubMed=1138922;
RA Wilkinson T., Chua C.G., Carrell R.W., Robin H., Exner T., Lee K.M.,
RA Kronenberg H.;
RT "A new haemoglobin variant, haemoglobin Camperdown (beta 104 (G6)
arginine-serine).";
RL Biochim. Biophys. Acta 393:195-200(1975).
RN [26]

Query Match 100%; Score 10; DB 1; Length 146;

Best Local Similarity 100%; Pred. No. 4; e-05; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LWVYPWTQRF 10
Db 32 LWVYPWTQRF 41

RESULT	54
ID	HBB_HVLLA
STANDARD	PRT;
PRT	146 AA.
AC	P02025;
DT	21-JUL-1985 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Hemoglobin beta chain.
GN	GN
OS	Hylobates lar (common gibbon).
OC	Eukaryota; Metzoa; Chorista; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarhini; Hylobatidae; Hylobates;
OX	NCBI_TAXID=9580;
RN	[11]
RP	SEQUENCE.
RX	MEDLINE=72020149; PubMed=4999925;
RA	Boyer S.H., Crosby E.F., Noyes A.N., Fuller G.F., Leslie S.E., Donaldson L.J., Vrablik G.R., Schaefer E.W. Jr., Thurmon T.F.;
RT	"primate hemoglobins: Some sequences and some proposals concerning the character of evolution and mutation.;" RL Blochim. Genet. 5:405-448(1971).
CC	-- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
CC	-- SUBUNIT: HETEROOTERAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC	-- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC	-- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR	PIR; A02355; HBG1.
DR	HSSP; P02023; IBBB.
DR	InterPro; IPR02337; Beta-haem.
DR	InterPro; IPR000971; Globin.
DR	Pfam; PF00042; globin_1.
DR	PRINTS; PRO0814; BETHAEM.
DR	PROSITE; PS01033; GLOBIN_1.
KW	Heme; Oxygen transport; Transport; Erythrocyte;
FT	POLYMORPHISM.
FT	METAL 63 63 IRON (HEME DISTAL LIGAND).
FT	METAL 92 92 IRON (HEME PROXIMAL LIGAND).
FT	VARIANT 80 80 N -> D (IN COMMON ALLELE).
FT	VARIANT 87 87 Q -> K (IN COMMON AND UNCOMMON ALLELE).
SQ	SEQUENCE 146 AA; 15925 MW; EACHC702CAD5BB4 CRC64;

Qy 1 LVVYPTQRF 10
 HBB_LEMVA STANDARD; PRT; 146 AA.
 ID HBB_LEMVA STANDARD; PRT; 146 AA.
 AC P02054;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DB 32 LVVYPTQRF 41
 DE Hemoglobin beta chain.
 GN HBB.
 OS Lemur catta (Ring-tailed lemur).
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemuridae; Lemur.
 OC NCBI_TAXID=9447;
 RN OX [1]
 RP SEQUENCE;
 RX MEDLINE=33185437; PUBMED=6841124;
 RA Coppenhaver D.H.; Dixon J.D.; Duffy L.K.;
 RT "Prosimian hemoglobins I. The primary structure of the beta-globin
 RT chain of Lemur catta.;"
 RL Hemoglobin 7:1-14(1983).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02371; HBLEC.
 DR HSSP: P0023;
 DR InterPro: IPR002337; Beta_haem.
 DR PROSITE: PS00814; BETAHARM.
 DR Pfam: PF0042; globin_1.
 DR PRINTS: PR00814; BETAHARM.
 DR PRINS: PS01033; GLOBIN_1.
 DR Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL_ 92 92 IRON (HEME DISTAL LIGAND).
 FT METAL_ 63 63 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15981 MW: EELIE98.B3DDB151 CRC64;

RESULT 55
 ID HBB_LEMVA STANDARD; PRT; 146 AA.
 AC P02054;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DR HBB.
 GN Lepus europaeus (European hare).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Lepus.
 OC NCBI_TAXID=9983;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87289065; PUBMED=3615213;
 RA Pauplin Y.; Rech J.;
 RT "Nucleotide sequence of hare adult beta-globin gene with flanking
 regions";
 RL Nucleic Acids Res. 15:5899-5899(1987).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 CC
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 DR EMBL: Y00347; CAA68429.1; -.
 DR PIR: A27101; A27101.
 DR HSSP: P02023;
 DR InterPro: IPR002337; Beta_haem.
 DR PROSITE: PS00814; BETAHARM.
 DR PRINTS: PR00814; BETAHARM.
 DR Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL_ 0 0 IRON (HEME DISTAL LIGAND).
 FT METAL_ 63 63 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15981 MW: EELIE98.B3DDB151 CRC64;

RESULT 56
 ID HBB_LEMVA STANDARD; PRT; 146 AA.
 AC P021667;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Lemur variegatus (Ruffed lemur) (Varecia variegata).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemuridae; Varecia.
 OC NCBI_TAXID=9455;
 RN [1]
 RP SEQUENCE;
 RA Duffy L.K.; Coppenhaver D.H.;
 RT "Prosimian hemoglobins II. Comparison of hemoglobin beta-chain primary
 structures in the genus Lemur.;"
 RL (In); Schneck A.G.; Paul C. (eds.);
 RL Brussels hemoglobin symposium, pp.377-392, Editions de l'Universite de

FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15931 MW; D9937E0F66281FDB CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 58
 HBB_LIPWPE STANDARD; PRT; 146 AA.

ID HBB_LIPWPE STANDARD; PRT; 146 AA.
 AC P15166;
 RT "Carnivora: the primary structure of the slender loris, *Loris tardigradus*.";
 DR "Amino acid sequences of the alpha and beta chains of adult hemoglobin of the slender loris, *Loris tardigradus*."
 RL J. Biochem. 84:377-383(1978).
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DR 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.
 GN HBB.
 OS Leptonychotes weddelli (Weddell seal).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidie; Leptonychotes.
 OC NCBI_TaxID=9713;
 OX RN [1]
 RP SEQUENCE.
 RX MEDLINE=89374816; PubMed=2775492;
 RA Lin H.-X.; Kleinschmidt T.; Braunitzer G.; weddelli, Pinnipedia) hemoglobin.";
 RT Biol. Chem. Hoppe-Seyler 370:713(1989).
 DR !- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
 CC !- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC !- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC !- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; S04952; HSILW.
 DR HSSP; P02023; 1BAB.
 DR InterPro; IPR00337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PROSITE; PRO0814; BETHAEM.
 DR PRINS; PS01033; GLOBIN_1.
 DR PROSITE; PS01033; GLOBIN_1.
 DR Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15900 MW; 10E3CA7C9580E22 CRC64;

RN [1]
 RP SEQUENCE.
 RX MEDLINE=89000194; PubMed=3166739;
 RA Lin H.-X.; Kleinschmidt T.; Braunitzer G.; Scheil H.-G.;
 RT "Carnivora: the primary structure of the common otter (*Lutra lutra*, Mustelidae) hemoglobin."
 RL Biol. Chem. Hoppe-Seyler 369:349-355(1988).
 DR !- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
 CC !- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC !- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC !- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; S00817; HBOT.
 DR HSSP; P02023; 1BAB.
 DR InterPro; IPR00337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PROSITE; PRO0814; BETHAEM.
 DR PROSITE; PS01033; GLOBIN_1.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15950 MW; 174C272C1DAE36A6 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 60
 HBB_LUTUJU STANDARD; PRT; 146 AA.

ID HBB_LUTUJU STANDARD; PRT; 146 AA.
 AC P10893;
 RT 01-JUL-1989 (Rel. 11, Created)
 DR 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN Lutra lutra (European river otter).
 OS Lutra lutra (European river otter).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae; lutra.
 OC NCBI_TaxID=9657;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=89000194; PubMed=3166739;
 RA Lin H.-X.; Kleinschmidt T.; Braunitzer G.; Scheil H.-G.;
 RT "Carnivora: the primary structure of the common otter (*Lutra lutra*, Mustelidae) hemoglobin."
 RL Biol. Chem. Hoppe-Seyler 369:349-355(1988).
 DR !- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
 CC !- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC !- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC !- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; S00817; HBOT.
 DR HSSP; P02023; 1BAB.
 DR InterPro; IPR00337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PROSITE; PRO0814; BETHAEM.
 DR PROSITE; PS01033; GLOBIN_1.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15950 MW; 174C272C1DAE36A6 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 61

ID HBB_LYNLY	STANDARD;	PRT;	146 AA.
AC P41338;			
DT 01-FEB-1995 (Rel. 31, Created)			
DT 01-FEB-1995 (Rel. 31, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE Hemoglobin beta chain.			
GN HBB.			
OS Lynx lynx (European lynx).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Lynx.			
OX NCBI_TaxID:13125;			
RN [1]			
RP SEQUENCE:			
RX MEDLINE=97384899; PubMed=1515033;			
RA Ahmed A., Jahan M., Braunzier G.;			
RT "Carnivora: the primary structure of the major hemoglobin component from adult European lynx (Lynx lynx, Felidae).";			
RL J. Protein Chem. 11:39-43 (1992).			
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.			
CC -1- SUBUNIT: HETEROOTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.			
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.			
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.			
DR PIR: B53880; B53880.			
DR HSSP: P02067; 1QPW.			
DR InterPro: IPR002337; Beta_haem.			
DR InterPro: IPR000971; Globin.			
DR Pfam: PF00042; globin_1.			
DR PRINTS: PR00814; BETAHAEM.			
DR PROSITE: PS01033; GLOBIN_1.			
DR PROSITE: PS01033; GLOBIN_1.			
KW Heme; Oxygen transport; Transport; Erythrocyte.			
FT METAL_ 63 63 IRON (HEME DISTAL LIGAND).			
FT METAL_ 92 92 IRON (HEME PROXIMAL LIGAND).			
FT METAL_ 92 92 IRON (HEME DISTAL LIGAND).			
SQ SEQUENCE 146 AA; 15925 MW; 98c53c3fa32fb8f2 CRC64;			

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 63

ID HBB_MACFU	STANDARD;	PRT;	146 AA.
AC P02027; O97SL4;			
DT 21-JUL-1986 (Rel. 01, Last sequence update)			
DT 01-MAR-2002 (Rel. 41, Last annotation update)			
DE Hemoglobin beta chain.			
GN HBB.			
OS Macaca fuscata fuscata (Japanese macaque), (Cynomolgus monkey), Macaca fascicularis (Crab eating macaque), and Macaca speciosa (Stump-tail macaque), and Macaca nemestrina (Pig tailed macaque).			
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.			
OC Macaca fascicularis (Crab eating macaque), and Macaca speciosa (Stump-tail macaque), and Macaca nemestrina (Pig tailed macaque).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.			
OX NCBI_TaxID:9543; 9541; 9553; 9545;			
RN [1]			
RP SEQUENCE:			
RC SPECIES=M_fuscata;			
RX MEDLINE=72030553; PubMed=5000512;			
RA Matuda G., Maita T., Ota H., Tachikawa I., Tanaka Y., Araya A., Nakashima Y.;			
RT "The primary structure of the beta-polypeptide chain of adult hemoglobin of the Japanese monkey (Macaca fuscata fuscata)."; Int. J. Protein Res. 3:53-55(1971).			
RT RT RT RT RT			
RL RNN [2]			
RP SEQUENCE:			
RC SPECIES=M_fascicularis;			
RX MEDLINE=7110403; PubMed=5459429;			
RT Wade P.T., Barnicot N.A., Huehns E.R.;			
RT "Structural studies on the major and minor haemoglobin of the monkey Macaca irus.";			
RT Biochim. Biophys. Acta 221:450-466(1970).			
RL RN [3]			
RP SEQUENCE OF 1-120 FROM N.A.			
RC SPECIES=M_fascicularis;			
RX MEDLINE=87254238; PubMed=3110424;			
RA Savatier P., Trabuchet G., Cheblounie Y., Faure C., Verdier G., Nigon V.M.;			
RT "Nucleotide sequence of the beta-globin genes in gorilla and macaque: the origin of nucleotide polymorphisms in human.";			
RX MEDLINE=87241983; PubMed=3593539;			

RL J. Mol. Evol. 24:309-318(1987).
 RN [4]
 RP SEQUENCE OF 106-146 FROM N.A.;
 SPECIES="M.fascicularis"; TISSUE=Blood;
 RX MEDLINE=20188801; PubMed=10723742;
 RA Francio M.P., Ochman H.;
 RT "Strand symmetry around the beta-globin origin of replication in
 primates";
 RL Mol. Biol. Evol. 17:416-422(2000).
 RN [5]
 RP SEQUENCE;
 SPECIES="M.speciosa";
 RC MEDLINE=8613127; PubMed=4091973;
 RA Maita T., Tanioka Y., Nakayama S., Matsuda G.;
 RT "Amino-acid sequences of the two major components of adult
 hemoglobins from the stump-tail monkey, *Macaca speciosa*";
 RL Biol. Chem. Hoppe-Seyler 366:1149-1154(1985).
 RN [6]
 RP SEQUENCE;
 SPECIES="M.nemestrina";
 RX MEDLINE=87299001; PubMed=3304337;
 RA Kleinschmidt T., Sgouras J.G.;
 RT "Hemoglobin sequences";
 RL Biol. Chem. Hoppe-Seyler 368:579-615(1987).
 RN [7]
 RP SEQUENCE;
 SPECIES="M.nemestrina";
 RX MEDLINE=74126665; PubMed=4206326;
 RA Nutt P.E., Patravas H.A.;
 RT "Amino acid compositions of the tryptic peptides comprising the beta-
 hemoglobin chain of *Macaca nemestrina*";
 RT Am. J. Phys. Anthropol. 40:75-82(1974);
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 CC This SWISS-PROT entry 1 copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; X05605; CAA29153.1; -.
 DR PIR; AAF2354; HBKG0R.
 DR PIR; A04622; HBKG0J.
 DR PIR; S10689; HBKG0M.
 DR PIR; C24693; C24693.
 DR HSSP; P01023; IBBAB.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000571; Globin.
 PRM; PF00042; globin_1.
 PRINTS; PRO0814; BETAHREM.
 PROSITE; PS01033; GLOBIN_1.
 DR Heme; Oxygen transport; Transport; Erythrocyte.
 FT INIT_MET 0 . IRON (HEME DISTAL LIGAND).
 FT METAL 63 63 . IRON (HEME PROXIMAL LIGAND).
 FT METAL 92 92 . IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 15983 MW; 56ADC1539B20955B C3C64;
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41
 RESULT 65
 HBB_MANSF STANDARD; PRM; 146 AA.
 ID HBB_MANSF
 AC P08259;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Mandrillus sphinx (Mandrill) (*Papio sphinx*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarhini; Cercopithecoidea;
 Cercopithecinae; Mandrillidae.
 OC Cercopithecinae; Mandrillidae.
 OX NCBI_TaxID=9561;
 RN [1]
 RP SEQUENCE;
 RX MEDLINE=88293710; PubMed=3401326;
 RA Lin H.-X., Kleinschmidt T., Braunitzer G., Goltenboch R.;
 RT "The primary structure of the mandrill (*Mandrillus sphinx*, Primates)
 hemoglobin";
 RT

RL Biol. Chem. Hoppe-Seyler 369:209-216(1988).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; S00540; HBBAM.
 DR HSSP; P02023; 1BAB.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PR0081; BEPAHAE.
 DR PROSITE; PS0103; 1.
 FT Heme; Oxygen transport; Transport; erythrocyte.
 METAL 63 IRON (HEME DISTAL LIGAND).
 FT METAL 63 IRON (HEME PROXIMAL LIGAND).
 FT SEQUENCE 146 AA; 15956 MW; 2CD5B86C7D708046 CRC64;
 SQ [1]
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; DE Hemoglobin beta chain.
 CC GN HBB.
 OS Megaderma lyra (Indian false vampire).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Megadermatidae;
 OC NCBI_TaxID=9413;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88163088; PubMed=3348887;
 RA Sgouras J.G., Kleinschmidt T., Braunitzer G.;
 RT "The primary structure of the hemoglobin of the Indian false vampire
 RL (Megaderma lyra, Microchiroptera);
 CC BIOL CHEM. HOPPE-SEYLER 369:47-53(1988).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; S00541; HBBTV.
 DR HSSP; P02023; 1ABW.
 DR InterPro; IPR00237; Beta_haem.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PR00814; BEPAHAE.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; erythrocyte.
 FT METAL 63 IRON (HEME DISTAL LIGAND).
 METAL 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 16145 MW; AD822D9385652470 CRC64;
 RN [1]
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; DE Hemoglobin beta chain.
 CC GN HBB.
 OS Mellivora capensis (Ratel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mellivorinae;
 OC Mellivora.
 OC NCBI_TaxID=9664;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=89207098; PubMed=3242544;
 RA Rodewald K., Braunitzer G., Goeltzenboch R.;
 RT "Carnivora: primary structure of the hemoglobins from ratel
 (Mellivora capensis)." ;
 RL BIOL CHEM. HOPPE-SEYLER 369:1137-1142(1988).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE

CC VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC KW
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; S01663; HBBDR.
 DR HSSP; P02023; 1BAB.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 DR KW Heme; Oxygen transport; Transport: Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 FT CONFLICT 50 52 SAS -> LPV (IN REF. 1).
 FT CONFLICT 115 115 S -> I (IN REF. 1).
 SQ SEQUENCE 146 AA; 15860 MW; FAAC582505A52C92 CRC64;

Query Match 100:0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVVPWTQRF 10
 Db 32 LVVVPWTQRF 41

RESULT 69
 HBB_MESAU STANDARD; PRT; 146 AA.

ID HBB_MESAU STANDARD; PRT; 146 AA.
 AC P02094;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta-major chain.
 HBB.
 GN Mesocricetus auratus (golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurogathi; Muridae; Cricetinae;
 OC NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92223120; PubMed=152610;
 RA Lee K.M., Subar M., Li H., Boussios T.;
 RT "Respiration at high altitudes, phosphoprotein interaction:
 sequence of the hemoglobins of the hamster (Mesocricetus aureatus) and
 the camel (Camelus ferus, Camelidae).";
 RL Biochim. Biophys. Acta 1130:343-344(1992).
 RN [2]
 RP SEQUENCE.
 RA Braunitzer G., Schrank B., Stangl A., Wiesner H.;
 RT "Cloning of two adult hamster globin cDNAs (alpha and beta major).";
 RL Chem. Soc. Pak. 2:1-7(1980).

DR HSSP; P02023; 1BAB.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 DR KW Heme; Oxygen transport; Transport: Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15935 MW; 046C273E1C83C98C CRC64;

Query Match 100:0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVVPWTQRF 10
 Db 32 LVVVPWTQRF 41

RESULT 70
 HBB_MUSLU STANDARD; PRT; 146 AA.
 AC P23502;
 DT 01-MOV-1991 (Rel. 20, Created)
 DT 01-MOV-1991 (Rel. 20, Last sequence update)
 DE Hemoglobin beta chain.
 HBB.
 OS Mustela lutreola (European mink).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 OC NCBI_TaxID=9666;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90303485; PubMed=2363790;
 RA Ahmed A., Jaham M., Braunitzer G.;
 RT "Carnivora: the amino acid sequence of the adult European mink
 (Mustela lutreola, Mustelidae) hemoglobins.";
 RL Z. Naturforsch. C 45:223-228(1990).
 DR PIR; S10105; HMNE.
 DR HSSP; P02023; 1BAB.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 DR KW Heme; Oxygen transport; Transport: Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15935 MW; 046C273E1C83C98C CRC64;

Query Match 100:0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVVPWTQRF 10
 Db 32 LVVVPWTQRF 41

RESULT 71
 HBB_MUSPF STANDARD; PRT; 146 AA.
 ID HBB_MUSPF
 AC P19017;
 DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 HBB.
 RN [1]
 RP SSEQUENCE.
 RX MEDLINE=87157093; PubMed=3828074;
 RA Kleinschmidt T.; Koop B.; Braunitzer G.;
 RT "The primary structure of a mouse-eared bat (*Myotis velifer*,
 Chiroptera) hemoglobin.", Biol. Chem. Hoppe-Seyler 367:1243-1249 (1986).
 RL -I- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 OC VARIOUS PERIPHERAL TISSUES.
 OS Mustela putorius (European polecat), Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 OX NCBI_TAXID=9669, 9668;
 RN [1]
 RP SSEQUENCE.
 RC SPECIES="M. p. furo";
 RA Pauplin Y., Hombrados I., Faure F., Han K.K., Neuzil E.;
 "The primary structure of the beta-chain of the haemoglobins of the
 ferret (Mustela putorius furo)", Biochem. Soc. Trans. 16:608-609(1988).
 RL [2]
 RN SEQUENCE.
 RC SPECIES="M. p. furo";
 RX MEDLINE=90121748; PubMed=2610931;
 RA Hombrados I., Vidal Y., Rodewald K., Braunitzer G., Neuzil E.;
 RT "Carnivora: the primary structure of the alpha-chains of ferret
 (Mustela putorius furo), Mustelidae) hemoglobins.", Biol. Chem., Hoppe-Seyler 370:1133-1138(1989).
 RL [3]
 RN SEQUENCE.
 RC SPECIES="M. putorius";
 RA Ahmed A., Jahan M., Braunitzer G., Peclhaner H.; European polecat
 RT (Mustela putorius, Mustelidae) hemoglobins., Naturforsch. C 44:817-824 (1989).
 RL -I- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -I- SUBUNIT: HETEROOTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -I- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: B25357; B25357.
 DR PROSITE: PS01033; GLOBIN; 1.
 DR HSSP: P02023; IBAB.
 DR Interpro; IPR00337; Beta_haem.
 DR Interpro; IPR00971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PRO0814; BETAHAE.
 DR PROSITE: PS01033; GLOBIN; 1.
 DR PIR; S11534; HBAN.
 DR S10103; HBKE.
 DR HSSP: P02023; IBAB.
 DR Interpro; IPR00337; Beta_haem.
 DR Interpro; IPR00971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PRO0814; BETAHAE.
 DR PROSITE; PS01033; GLOBIN; 1.
 DR Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SO SEQUENCE 146 AA; 15994 MW; DC99326ED2F4DBA4 CRC64;

RESULT ?3

Query Match ID	HBB_NASNA	Best Local Similarity	Score 10;	PRT; 146 AA.
Qy	P26916;	100.0%; Pred. No. 4.2e-05;	DB 1;	Length 146;
Matches	10;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Db	32	LVVPWTQRF 41		

Query Match ID HBB_NASNA STANDARD; PRT; 146 AA.

OX NCBI_TAXID=9435;
 RN [1]
 RP SSEQUENCE.
 RX MEDLINE=90253580; PubMed=2340073;
 RA Ahmed A., Jahan M., Braunitzer G.;
 RT "Carnivora: the primary structure of hemoglobin from adult coati (Nasua nasua rufa, Procyonidae).", J. Protein Chem. 9:23-29(1990).
 RL -I- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 OC VARIOUS PERIPHERAL TISSUES.
 CC -I- SUBUNIT: HETEROOTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -I- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: B39020; B39020.
 DR HSSP; P02023; IBAB.
 DR Interpro; IPR00337; Beta_haem.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PRO0814; BETAHAE.
 DR PROSITE; PS01033; GLOBIN; 1.
 FT Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 SO SEQUENCE 146 AA; 16077 MW; E3FC1B20657EA57 CRC64;

RESULT ?2

HBB_MYOVE ID	HBB_MYOVE STANDARD; PRT; 146 AA.
AC P11758;	
DT 01-OCT-1989 (Rel. 12, Created)	
DT 01-OCT-1989 (Rel. 12, Last sequence update)	
DT 16-OCT-2001 (Rel. 40, Last annotation update)	
DE Hemoglobin beta chain.	
GN HBB.	
OS Myotis velifer (Mouse-eared bat).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chiroptera; Microchiroptera; Vespertilionidae; Myotis.	

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Mismatches 0; Indels 0; Gaps 0; Ondatra zibethicus (Muskrat).
 Qy 1 LVVYPWTORF 10
 Db 32 LVVYPWTORF 41

RESULT 74
 HBB_NYCCO STANDARD: PRT; 146 AA.
 ID HBB_NYCCO
 AC P02049;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Nycticebus coucang (Slow loris).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Nycticebus.
 OX NCBI_TaxID=9470;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=4115165; PubMed=4782642;
 RA Matsuda G., Maita T., Watanabe B., Ota H., Araya A., Goodman M., Psychodo W.;
 RT "The primary structures of the alpha and beta polypeptide chains of adult hemoglobin of the slow loris (*Nycticebus coucang*).", INT. J. Pept. Protein Res. 5:419-421(1973).
 RL -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 DR PIR: P02023; IBAB.
 DR InterPro: IPR00971; Globin.
 DR Pfam: PF00042; globin_1.
 DR PRINTS: PR00314; BETAHBEM.
 DR PROSITE: PS01033; GLOBIN_1.
 DR PIR: P0356; HBLBS.
 DR HSSP; P02023; IBAB.
 DR InterPro: IPR00971; Globin.
 DR Pfam: PF00042; globin_1.
 DR PRINTS: PR00314; BETAHBEM.
 DR PROSITE: PS01033; GLOBIN_1.
 DR Heme; Oxygen transport; Transport; Erythrocyte.
 KW METAL 63 IRON (HEME DISTAL LIGAND).
 FT METAL 63 IRON (HEME PROXIMAL LIGAND).
 FT METAL 92 IRON (HEME DISTAL LIGAND).
 FT METAL 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA: 15900 MW; FEE3CA7AE75A8026 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Mismatches 0; Indels 0; Gaps 0; Ondatra zibethicus (Muskrat).
 Qy 1 LVVYPWTORF 10
 Db 32 LVVYPWTORF 41

RESULT 75
 HBB_ONDZI STANDARD: PRT; 146 AA.
 ID HBB_ONDZI
 AC P02093;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OC Ondatra zibethicus (Muskrat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Arvicolinae; Ondatra.
 OX NCBI_TaxID=10060;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=4110063; PubMed=6363267;
 RA Bieber F.A., Braunitzer G.;
 RT "Primary structure of hemoglobins of the musk rat (*Ondatra zibethica*, Rodentia).", Hoppe Seyler's Z. Physiol. Chem. 364:1527-1536(1983).
 RN [2]
 RP REVISION TO 39.
 RX MEDLINE=87299001; PubMed=3304337;
 RA Bieber F.A., Braunitzer G.;
 RL Unpublished results, cited by:
 RL Kleinschmidt T., Sgourou J.G.;
 RL Biol. Chem. Hoppe-Seyler 368:579-615(1987).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC	-I- TISSUE SPECIFICITY: BELONGS TO THE GLOBIN FAMILY.	AC	HBB_PAGLA	STANDARD;	PRT;	146 AA.
PIR:	AQ08149; HBOZ.	DR	P19546;			
DR	HSSP; P02067; 1QPN.	DT	01-FEB-1991 (Rel. 17, Created)			
DR	InterPro; IPR02337; Beta-haem.	DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DR	InterPro; IPR000571; Globin.	DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DR	pFam; PF00042; globin_1.	DE	Hemoglobin beta chain.			
DR	PRINTS; PR00814; BETAHBEM.	RN	HBB.			
DR	Heme; Oxygen transport; Transport; Erythrocyte.	OS	Paguma larvata (Masked palm civet).			
KW	Mammalia; Etheria; Carnivora; Fissipedia; Paguma.	OC	Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;			
FT	METAL	OX	Mammalia; Etheria; Carnivora; Fissipedia; Paguma.			
FT	METAL	NCBI_TaxID:9675;				
SQ	SEQUENCE	[1]				
RESULT	77	RP	SEQUENCE.			
HBB_ORVAN	STANDARD;	RA	Medline=91166740; PubMed=2076197;			
ID	PRT;	RT	He C., Braunitzer G., Goeltzenbohr R.;			
AC	146 AA.	RT	Carnivora: the primary structure of hemoglobin from the Masked palm			
DT	PO2111;	RT	civet (Paguma larvata, Viverridae).;			
DT	21-JUL-1986 (Rel. 01, Created)	RL	Biol. Chem. Hoppe-Seyler 371:15201990).			
DT	21-JUL-1986 (Rel. 01, Last sequence update)	CC	-I- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE			
DT	16-OCT-2001 (Rel. 40, Last annotation update)	CC	VARIOUS PERIPHERAL TISSUES.			
DE	Hemoglobin beta chain.	CC	-I- SUBUNIT: HETEROOTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.			
HBB	O S	CC	-I- TISSUE SPECIFICITY: RED BLOOD CELLS.			
Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.	OC	CC	-I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.			
OC	NCBI_TaxID:9258;	DR	PRINTS; PR00814; BETAHBEM.			
RN	[1]	DR	P13281; S13281.			
RP	SEQUENCE.	DR	RHSSP; P02023; 1QAB.			
RX	MEDLINE=76061123; PubMed=191127;	DR	IntarPro; IPR002337; Beta-haem.			
RA	Whittaker R.G., Thompson E.O.P.;	DR	IntarPro; IPR000571; Globin.			
CC	Studies on monocrome proteins. VI. Amino acid sequence of the beta-	DR	pFam; PF00042; globin_1.			
RT	chain of haemoglobin from the Platypus, Ornithorhynchus anatinus.";	DR	PRINTS; PR00814; BETAHBEM.			
RL	Aust. J. Biol. Sci. 28:353-365(1975).	DR	P13281; S13281.			
CC	-I- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE	DR	RHSSP; P02023; 1QAB.			
CC	VARIOUS PERIPHERAL TISSUES.	DR	IntarPro; IPR002337; Beta-haem.			
-I- SUBUNIT: HETEROOTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.	CC	DR	InterPro; IPR000571; Globin.			
-I- TISSUE SPECIFICITY: RED BLOOD CELLS.	CC	DR	pFam; PF00042; globin_1.			
-I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.	CC	DR	PRINTS; PR00814; BETAHBEM.			
PIR; A02431; HBOZ.	DR	DR	P13281; S13281.			
HSSP; P02023;	DR	DR	RHSSP; P02023; 1QAB.			
InterPro; IPR002337; Beta-haem.	DR	DR	IntarPro; IPR000571; Globin.			
InterPro; IPR000571; Globin.	DR	DR	PRINTS; PR00814; BETAHBEM.			
PFAM; PF00042; globin_1.	DR	DR	P13281; S13281.			
PRINTS; PR00814; BETAHBEM.	DR	DR	RHSSP; P02023; 1QAB.			
DR	Heme; Oxygen transport; Transport; Erythrocyte.	DR	IntarPro; IPR002337; Beta-haem.			
Mammalia; Metacozoa; Chordata; Craniata; Vertebrates; Euteleostomi;	OC	DR	InterPro; IPR000571; Globin.			
Heme; Oxygen transport; Transport; Erythrocyte.	OC	DR	pFam; PF00042; globin_1.			
METAL	FT	DR	PRINTS; PR00814; BETAHBEM.			
METAL	FT	DR	P13281; S13281.			
SEQUENCE	SQ	DR	RHSSP; P02023; 1QAB.			
146 AA;	146 AA;	DR	IntarPro; IPR000571; Globin.			
15872 MW;	16011 MW;	DR	PRINTS; PR00814; BETAHBEM.			
E9043FFEC82ADB2E1 CRC64;		DR	P13281; S13281.			
RESULT	79	Query Match	100.0%; Score 10; DB 1; Length 146;			
CC	Best Local Similarity 100.0%; Pred. No. 4.2e-05;	Best Local Similarity 100.0%; Pred. No. 4.2e-05;				
Matches	10;	Matches	0;			
CC	Conservative 0;	Conservative 0;				
CC	Mismatches 0;	Mismatches 0;				
CC	Indels 0;	Indels 0;				
CC	Gaps 0;	Gaps 0;				
CC	SEQUENCE	SEQUENCE.				
CC	146 AA;	146 AA;				
CC	15872 MW;	16011 MW;				
CC	E9043FFEC82ADB2E1 CRC64;					
Query Match	100.0%; score 10; DB 1; Length 146;	Query Match	100.0%; score 10; DB 1; Length 146;			
Best Local Similarity 100.0%; Pred. No. 4.2e-05;	Best Local Similarity 100.0%; Pred. No. 4.2e-05;	Best Local Similarity 100.0%; Pred. No. 4.2e-05;				
Matches 10;	Matches 10;	Matches 10;				
CC	Conservative 0;	Conservative 0;				
CC	Mismatches 0;	Mismatches 0;				
CC	Indels 0;	Indels 0;				
CC	Gaps 0;	Gaps 0;				
CC	SEQUENCE	SEQUENCE.				
CC	146 AA;	146 AA;				
CC	15872 MW;	16011 MW;				
CC	E9043FFEC82ADB2E1 CRC64;					
RESULT	78	RP	Abbas A., Braunitzer G.;			
HBB_PAGLA	RT	"The primary structure of haemoglobin from amur-leopard (Panthera				
RT	RT	pardus orientalis)".				
RL	J. Protein Chem. 4:57-67(1985);	J. Protein Chem. 4:57-67(1985);				
CC	-I- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE	CC	FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE			
CC	VARIOUS PERIPHERAL TISSUES	CC	VARIOUS PERIPHERAL TISSUES			
CC	-I- SUBUNIT: HETEROOTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.	CC	-I- SUBUNIT: HETEROOTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.			
CC	Miscellaneous: In the cat family (felidae), the oxygen affinity of	CC	Miscellaneous: In the cat family (felidae), the oxygen affinity of			
CC	hemoglobin depends little or not at all on the association with	CC	hemoglobin depends little or not at all on the association with			
CC	Diphosphoglycerate (DPG).	CC	Diphosphoglycerate (DPG).			
CC	-I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.	CC	-I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.			
DR	PIR; A02373; HBOZ.	DR	PIR; A02373; HBOZ.			

DR HSSP; P02067; 1OPW.
 DR InterPro; IPR02337; Beta_haem.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PRO0814; BEPAHAEV.
 DR PROSITE; PS01033; GLOBIN_1.
 DR Heme; Oxygen transport; Transport; Erythrocyte;
 KW Acetylation.
 MOD_RES 1 1 ACETYLATION.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 15986 MW; FAB18B0F2C94866E5 CRC64;
 SQ

Query Match 100 %; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 80
 HBB_PANTS STANDARD; PRT; 146 AA.
 ID HBB_PANTS
 AC P1084;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update),
 DE Hemoglobin beta-1 and beta-2 chains.
 GN HBB.
 OS Panthera tigris sumatrae (Sumatran tiger),
 OS Panthera leo (Lion), and
 OS Panthera pardus saxicolor (Northern persian leopard).
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Pantheridae; Euteleostomi;
 OC NCBIL_TaxID=9695, 9690, 9689, 9693;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P_t.sumatrae;
 RX MEDLINE=89228545; PubMed=2713095;
 RA Jahan M.J., Ahmed A., Braunitzer G., Goeltenboth R.;
 RT "Carnivora: the amino-acid sequence of the adult Sumatran tiger
 (Panthera tigris sumatrae) hemoglobins.";
 RL Biol. Chem. Hoppe-Seyler 370:27-33(1989).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P_onca;
 RX MEDLINE=88107004; PubMed=3426807;
 RA Ahmed A., Jahan M., Zaidi Z.H., Braunitzer G., Goeltenboth R.;
 RT "The primary structure of the hemoglobins of the adult jaguar
 (Panthera onca, Carnivora).";
 RL Biol. Chem. Hoppe-Seyler 368:1385-1390(1987).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=P_leo;
 RA Jahan M., Ahmed A., Braunitzer G., Zaidi Z.H., Goeltenboth R.;
 RT "Carnivora: the primary structures of adult lion (Panthera leo)
 hemoglobins.";
 RL Naturforsch. C 42:1465-1470(1987).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=P_saxicolor;
 RA Ahmed A., Jahan M., Braunitzer G., Goeltenboth R.;
 RT "Carnivora: the primary structure of the major and minor hemoglobin
 components of adult north persian leopard (Panthera pardus
 sexicolor).";
 RT Naturforsch. C 43:1341-1346(1988).
 -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 -!- SUBUNIT: HETEROOTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; A04624; HBBAV.
 DR HSSP; P02023; 1BAB.
 DR InterPro; IPR00337; Beta_haem.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PRO0814; BEPAHAEV.
 DR PROSITE; PS01033; GLOBIN_1.
 DR Heme; Oxygen transport; Transport; Erythrocyte.
 FT HMM; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 15895 MW; FOBEB0778B0CF413 CRC64;

CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- MISCELLANEOUS: IN THE CAT FAMILY (FELIDAE), THE OXYGEN AFFINITY OF
 HEMOGLOBIN DEPENDS LITTLE OR NOT AT ALL ON THE ASSOCIATION WITH
 DIPHOSPHOGLYCERATE (DPG).
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 CC PIR; S00522; HBATU.
 DR PIR; S02079; HBTX1.
 DR PIR; S11301; HBWX2.
 DR PIR; S03925; HBTEL.
 DR PIR; S03926; HBBD1P.
 DR PIR; S03929; HBBD2P.
 DR HSSP; P02067; 1OPW.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PRO0814; BEPAHAEV.
 DR PROSITE; PS01033; GLOBIN_1.
 DR Heme; Oxygen transport; Transport; Erythrocyte;
 KW Acetylation.
 MOD_RES 1 1 ACETYLATION.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 15986 MW; A128EA70467DB837 CRC64;
 SQ

Query Match 100 %; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 81
 HBB_PAPCY STANDARD; PRT; 146 AA.
 ID HBB_PAPCY
 AC P02030;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update),
 DE Hemoglobin beta chain.
 GN HBB.
 OS Papio cynocephalus (Yellow baboon);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 OC Mammalia; Buteria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopithecinae; Papio.
 OC NCBI_TaxID=9556;
 RX [1]
 RP SEQUENCE.
 RX MEDLINE=80227364; PubMed=7390858;
 RA Nutt; P.E., Mahoney W.C.;
 RT "Complete primary structure of the beta chain from the hemoglobin of
 a baboon, Papio cynocephalus.";
 RT RL Hemoglobin 4:109-123(1980).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROOTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; A04624; HBBAV.
 DR HSSP; P02023; 1BAB.
 DR InterPro; IPR00337; Beta_haem.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PRO0814; BEPAHAEV.
 DR PROSITE; PS01033; GLOBIN_1.
 DR Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 15895 MW; FOBEB0778B0CF413 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; RA
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVVPWTQRF 10
 Db 32 LVVVPWTQRF 41

RESULT 82

HBB_PHOVT STANDARD; PRT; 146 AA.

ID HBB_PHOVT
 AC P03909;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.

GN HBB.
 OS Phoca vitulina (Harbor seal).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
 OX NCBI_TaxID=9720;
 RN [1]

SEQUENCE:
 MEDLINE-87157094; PubMed=3828075;
 Watsonabe B., Maita T., Matsuda G., Goodman M., Johnson M.L.;
 "Amino-acid sequence of the alpha and beta chains of adult hemoglobin
 of the harbor seal," Phoca vitulina." Biol. Chem. Hoppe-Seyler 367:1251-1258(1986).
 RL -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 CCRP: B25358; B25358.
 DR PROSITE: PS01033; GLOBIN: 1.
 DR Heme; Oxygen transport; Transport; Erythrocyte;
 DR InterPro: IPR002337; Beta_haem.
 DR Pfam: PF0042; globin; 1.
 DR PRIMIS; PR00814; BETAHABM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 92 92 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 2 2 H -> O (IN BETA-I).
 FT VARIANT 5 5 G -> A (IN BETA-I).
 FT VARIANT 11 11 L -> V (IN BETA-I).
 SQ SEQUENCE 146 AA; 16184 MW; 6G65A2BADEAE656 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; RA
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVVPWTQRF 10
 Db 32 LVVVPWTQRF 41

RESULT 84

HBB_PIG STANDARD; PRT; 146 AA.

ID HBB_PIG
 AC P02667; Q29025;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.

GN HBB.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]

SEQUENCE FROM N.A.
 RA Sharmin A., Parson C.T., Midha S., Okabe J., Yerle M., Pinton P.,
 RA Lozan J., Kumar L.R.;
 RA Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

RESULT 83

HBB_PHYCA STANDARD; PRT; 146 AA.

ID HBB_PHYCA
 AC P09505;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta-I and beta-II chains.

GN HBB.
 OS Physeter catodon (Sperm whale) (Physeter macrocephalus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; odontoceti;
 OC Physeteridae; Physeter.
 OX NCBI_TaxID=9755;
 RN [1]

SEQUENCE.

RX MEDLINE-86242695; PubMed=3718676;
 RA Abbott A., Braunitzer G., Matsuda G., Maita T.;
 RT "The primary structure of sperm whale hemoglobin (Physeter catodon,
 cetacea)." Biol. Chem. Hoppe-Seyler's Z. Physiol. Chem. 359:137-146(1978).

RX MEDLINE-9508021; PubMed=7980139;
 RA Katz D.S., White S.P., Huang W., Kumar R., Christianson D.W.;
 RT "Structure determination of aquomet porcine hemoglobin at 2.8-A
 resolution." J. Mol. Biol. 244:541-553(1994).

RX MEDLINE-20180433; PubMed=10713517;
 RA Lu T.-H., Panneerselvam K., Liaw Y.-C., Kan P., Lee C.-J.,

RT "Structure determination of porcine haemoglobin.";
 RL Acta Crystallogr. D 56:304-312(2000);
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

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EMBL; X86791; CAA60490.1; -.
 DR PIR; A02385; HBPC.
 DR PDB; 2PGH; 30-NOV-94.
 DR IOPW; 04-JUN-99.
 DR InterPro; IPR002337; Beta_haem.
 DR IPR000971; Globin.
 PFAM; PF00042; globin_1.
 PRINTS; PRO0814; BETAHAE.
 PROSITE; PS01033; GLOBIN_1.
 DR Heme; Oxygen transport; Transport; Erythrocyte;
 KW 3D-structure.
 FT INIT_MET 0 0
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 FT CONFLICT 125 125 N -> D (IN REF. 2). CRC64;
 FT SQUENCE 146 AA; 16034 MW; B54203A32PDDC93 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; gaps 0;
 Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 85
 HBB__PREN STANDARD; PRT; 146 AA.
 ID HBB__PREN
 AC P02032;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 HBB.
 OS Proteles cristatus (Aardwolf). Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Hyaenidae; Proteles.
 OC NCBI_TaxID=9680;
 OX RN [1]
 RP SQUENCE.
 RX MEDLINE=92000305; PubMed=1910578;
 RA Stoeva S., Kleinschmidt T., Braunitzer G., Scheil H.-G.;
 RT "The primary structure of the hemoglobin from the aardwolf (Proteles cristatus, Hyaenidae)." Biol. Chem. Hoppe-Seyler 372:393-399(1991).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROCTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

InterPro; IPR002337; Beta_haem.
 DR PIR; SF6110; SF6110.
 HSSP; P02023; IBAB.
 DR InterPro; IPR000971; Globin.
 DR PF00042; globin_1.
 PRINTS; PRO0814; BETAHAE.
 PROSITE; PS01033; GLOBIN_1.
 DR Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQUENCE 146 AA; 15987 MW; E94D81F73B129834 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; gaps 0;
 Qy 1 LVVYPWTQRF 10
 Db 32 LVVYPWTQRF 41

RESULT 87
 HBB__PROA STANDARD; PRT; 146 AA.
 ID HBB__PROA
 AC P02086;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.
 HBB.
 GN Procvia capensis habessinica (Abyssinian hyrax).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Hyracidae; Procavidae; Procvavia.
 OC NCBI_TAXID=9814;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=84030514; PubMed=6623339;
 RA Kleinschmidt T., Braunitzer G.;
 RT "The primary structure of hemoglobins of the rock hyrax (Procvavia
 habessinica, Hyracoidea): insertion of glutamine in the alpha
 chains.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:1303-1313(1983).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 PIR: A02402; HBKB.
 HSSP: P02023; IBAB.
 InterPro: IPR002337; Beta_haem.
 InterPro: IPR000971; Globin.
 Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 DR Heme; Oxygen transport; Erythrocyte; Acetylation.
 FT MOD_RES 1 1 ACETYLATION (IN 20% OF THE CHAINS).
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 16205 MW; 1045D760101DBEC1 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 69
 ID HBB_PTEAL
 ID HBB_PTEAL STANDARD; PRT; 146 AA.
 AC P11391;
 DT 01-JAN-1990 (Rel. 13, created)
 DT 01-JAN-1990 (Rel. 13, last sequence update)
 DT 16-CCT-2001 (Rel. 40, last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Pteropus alecto (Black flying fox);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
 OC NCBI_TAXID=9402;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=89149963; PubMed=3228493;
 RA Kleinschmidt T., Sgouras J.G., Pettigrew J.D., Braunitzer G.;
 RT "The primary structure of the hemoglobin from the grey-headed flying
 fox (Pteropus poliocephalus) and the black flying fox (P. alecto,
 Megachiroptera).";
 RL Biol. Chem. Hoppe-Seyler 369:975-984(1988).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S01309; HBFBX.
 DR HSSP: P02023; IBAB.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 DR Heme; Oxygen transport; Transport; Erythrocyte;
 KW Polymorphism.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 139 139 N->T
 SQ SEQUENCE 146 AA; 15937 MW; FC0590DR35543643 CRC64;

RESULT 88
 ID HBB_PROLO
 ID HBB_PROLO STANDARD; PRT; 146 AA.
 AC P18889;
 DT 01-NOV-1990 (Rel. 16, created)
 DT 01-Nov-1990 (Rel. 16, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 Procyon lotor (Raccoon).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Procyon.
 OC NCBI_TAXID=9654;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=9026631; PubMed=701090;
 RA Brimhall B., Stangland K., Jones R.T., Becker R.R., Bailey T.J.;
 RT "Amino acid sequence of the hemoglobin of raccoon (Procyon lotor).";
 RL Hemoglobin 21:351-350(1978).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 PIR: S0625; HBRR.
 DR P02023; IBAB.
 DR InterPro: IPR00337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 PROSITE: PS01033; GLOBIN; 1.

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 93
 ID HBB_PTEBR
 ID HBB_PTEBR STANDARD; PRT; 146 AA.
 AC P10836;
 DT 01-JUL-1989 (Rel. 11, created)
 DT 01-JUL-1989 (Rel. 11, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)

DE Hemoglobin beta chain.
 GN HBB.
 OS Pteronura brasiliensis (Giant otter), and
 Martes foina (Beach marten).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
 OC Pteronura.
 OC NCBI_TaxID=9672, 9659;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.brasiiliensis;
 RX MEDLINE=89228546; PubMed=2713096;
 RA Kleinschmidt T., Braunitzer G., Scheil H.-G.;
 RT "Carnivora: the primary structure of the giant otter (Pteronura
 basiliensis, Mustelidae) hemoglobin.";
 RL Biol. Chem. Hoppe-Seyler 370:35-40(1989).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=M.foina;
 RX MEDLINE=90359058; PubMed=2390216;
 RA Ruecknagel K.P., Wiesner H., Braunitzer G.;
 RT "Carnivora: the primary structure of the beach marten (Martes foina,
 Mustelidae) hemoglobin.";
 RL BIOL. CHEM. HOPPE-SEYLER 371:503-509(1990).
 CC -I- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -I- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -I- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S02281; HBORG.
 DR PIR: S10599; HBDBM.
 DR HSSP; P02023; IBBB.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 PRIM: PF00042; globin_1.
 DR PRINTS: PRO0814; BETAHBEM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 KW Polymorphism.
 FT METAL; 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 15934 MW; 4D4C273AC7A08CBE CRC64;
 SQ PRT: S10599;
 DR HSSP; P02023; IBBB.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR PRINTS: PRO0814; BETAHBEM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 KW Polymorphism.
 FT METAL; 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 15934 MW; 4D4C273AC7A08CBE CRC64;
 SQ PRT: S10599;
 DR HSSP; P02023; IBBB.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR PRINTS: PRO0814; BETAHBEM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 KW Polymorphism.
 FT METAL; 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 15934 MW; 4D4C273AC7A08CBE CRC64;
 SQ PRT: S10599;
 DR HSSP; P02023; IBBB.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR PRINTS: PRO0814; BETAHBEM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 KW Polymorphism.
 FT METAL; 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 15934 MW; 4D4C273AC7A08CBE CRC64;
 SQ PRT: S10599;
 DR HSSP; P02023; IBBB.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR PRINTS: PRO0814; BETAHBEM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 KW Polymorphism.
 FT METAL; 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 15934 MW; 4D4C273AC7A08CBE CRC64;
 SQ PRT: S10599;
 DR HSSP; P02023; IBBB.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR PRINTS: PRO0814; BETAHBEM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 KW Polymorphism.
 FT METAL; 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 15934 MW; 4D4C273AC7A08CBE CRC64;
 SQ PRT: S10599;
 DR HSSP; P02023; IBBB.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR PRINTS: PRO0814; BETAHBEM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 KW Polymorphism.
 FT METAL; 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 15934 MW; 4D4C273AC7A08CBE CRC64;
 SQ PRT: S10599;
 DR HSSP; P02023; IBBB.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR PRINTS: PRO0814; BETAHBEM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 KW Polymorphism.
 FT METAL; 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 15934 MW; 4D4C273AC7A08CBE CRC64;
 SQ PRT: S10599;
 DR HSSP; P02023; IBBB.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR PRINTS: PRO0814; BETAHBEM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 KW Polymorphism.
 FT METAL; 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 15934 MW; 4D4C273AC7A08CBE CRC64;
 SQ PRT: S10599;
 DR HSSP; P02023; IBBB.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR PRINTS: PRO0814; BETAHBEM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 KW Polymorphism.
 FT METAL; 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 15934 MW; 4D4C273AC7A08CBE CRC64;
 SQ PRT: S10599;
 DR HSSP; P02023; IBBB.
 DR InterPro; IPR002337; Beta-haem.
 DR InterPro; IPR000971; Globin.
 DR PRINTS: PRO0814; BETAHBEM.
 DR PROSITE; PS01033; GLOBIN_1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 KW Polymorphism.
 FT METAL; 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 SEQUENCE 146 AA; 15934 MW; 4D4C273AC7A08CBE CRC64;

RX	MEDLINE=80132479; PubMed=7357610;
RA	pavlikis G.N.; Lockard R.E.; Vamvakopoulos N.; Rieser L.,
RA	Rajbhandary U.L.; Vourakis J.N.;
RT	"Secondary structure of mouse and rabbit alpha- and beta-globin mRNAs: differential accessibility of alpha and beta initiator AUG codons towards nucleases.";
RT	Cell 19:91-102(1980).
[6]	OCCURRENCE AND FREQUENCY OF ALLELIC CHAINS.
RN	MEDLINE=75031122; PubMed=4530669;
RX	Garrick M.D.; Hafner R.; Bricker J.; Garrick L.M.;
"Genetic variation in the primary structure of the beta chain of rabbit hemoglobin";	
RN	Aun. N.Y. Acad. Sci. 241:436-438(1974).
[7]	SEQUENCE FROM N.A. (BETA-2).
RN	MEDLINE=80030069; PubMed=516769;
RX	Hardison R.C.; Butler E.T. III; Lacy E.; Maniatis T.; Rosenthal N.,
RA	Efstathiadis A.;
RN	"The structure and transcription of four linked rabbit beta-like globin genes.>";
RL	Cell 18:1265-1297(1979).
[8]	SEQUENCE FROM N.A. (BETA-2).
RX	MEDLINE=89178632; PubMed=2486295;
RA	Margot J.B.; Demers G.W.; Hardison R.C.;
RT	"Complete nucleotide sequence of the rabbit beta-like globin gene cluster. Analysis of intergenic sequences and comparison with the human beta-like globin gene cluster.";
RL	J. Mol. Biol. 205:15-40(1989).
[9]	SEQUENCE OF 99-114 FROM N.A. (BETA-1).
RX	MEDLINE=79114395; PubMed=264241;
RA	van den Berg J.; van Ooyen A.; Mantel N.; Schamboeck A.; Grosveld G.,
RA	Flavell R.A.; Weissmann C.;
RT	"Comparison of cloned rabbit and mouse beta-globin genes showing strong evolutionary divergence of two homologous pairs of introns.";
RL	Nature 276:347-47(1978).
-	- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
-	- HETEROGENEITY: HETERTRIMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
-	- TISSUE SPECIFICITY: RED BLOOD CELLS.
-	- POLYMORPHISM: THERE ARE TWO ALLELES. THE SEQUENCE SHOWN IS THAT OF BETA-1; THE MOST FREQUENT OF THE TWO COMMON ALLELES.
-	- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; J00660; AAA31274.1; --.
DR	EMBL; J00882; CNA24251.1; --.
DR	EMBL; M18918; AAA02985.1; --.
DR	EMBL; V00878; CNA24247.1; --.
DR	EMBL; V00879; CNA24248.1; --.
DR	EMBL; M10843; AAA31270.1; --.
DR	EMBL; K03256; AAA31277.1; --.
DR	EMBL; M10525; AAA31268.1; --.
DR	EMBL; M10831; AAA31271.1; --.
DR	EMBL; J00659; AAA31273.1; --.
DR	EMBL; M10833; AAA31272.1; --.
DR	EMBL; M10832; AAA31272.1; JOINED.
PIR	A02375; HBHB.
PIR	S03090; S03090.
DR	HSSP; P02203; 1BAB.
DR	InterPro; IPR00337; Beta-haem.
DR	InterPro; IPR00971; Globin.
DR	Pfam; PF0002; globin; 1.
PRINS	PR00814; BETAHBEM.

ID HBB_ROUAE STANDARD; PRT; 146 AA.
 AC P02058;
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 HBB.
 OS Roussettus aegyptiacus (Egyptian rousette) (Egyptian fruit bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodida;
 Pteropodinae; Roussettus.
 OX NCBI_TaxID=9407;
 RN [1]
 RP SEQUENCE:
 MEDLINE=33055089; PubMed=7141404;
 RX
 RA Kleinschmidt T.; Braunitzer G.;
 RT "Primary structure of the hemoglobins from the Egyptian fruit bat (Roussettus aegyptiacus, Chiroptera)." ;
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1209-1215(1982).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROOTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; A02376; HBTF.
 DR HSSP; P02023; IBAB.
 DR InterPro; IPR002337; Beta_haem.
 DR IntePro; IPR002337; Beta_haem.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS0103; GLOBIN_1.
 DR METAL; 63 63 IRON (HEME DISTAL LIGAND).
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15914 MW; ELC5946CFE060DB7 CRC64;
 DR HBB_SAGMY STANDARD; PRT; 146 AA.
 AC P02038;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Saguinus mystax (Moustached tamarin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
 OX NCBI_TaxID=9488;
 RN [1]
 RP SEQUENCE:
 RX MEDLINE=72020149; PubMed=499925;
 RA Boyer S.H., Crosby E.F., Noyes A.N., Fuller G.F., Leslie S.E.,
 Donaldson L.J., Vrablik G.R., Schaefer E.W. Jr., Thurmon T.F.;
 RT "Primary hemoglobins: Some sequences and some proposals concerning the character of evolution and mutation." ;
 RL Biochem. Genet. 5:405-448(1977).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROOTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; A02350; HBMM.
 DR HSSP; P02023; IBAB.
 DR InterPro; IPR002337; Beta_haem.
 DR IntePro; IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS0103; GLOBIN_1.
 DR METAL; 63 63 IRON (HEME DISTAL LIGAND).
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15958 MW; 57EAB8B694579C93 CRC64;
 DR HBB_SAGNT STANDARD; PRT; 146 AA.
 AC P02037;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 HBB.
 OS Saguinus fuscicollis (Brown-headed tamarin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
 OX NCBI_TaxID=9487;
 RN [1]
 RP SEQUENCE:
 MEDLINE=7021459; PubMed=823937;
 RX
 RA Lin K.D., Kim Y.K., Chernoff A.I.;
 RT "Primary structure of the marmoset (Saguinus fuscicollis) hemoglobin. I. Use of tryptic maleylated peptides in the solubilization and sequence elucidation of the alpha- and beta-chains." ;
 RL Biochem. Genet. 14:427-440(1976).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROOTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; A02350; HBMQF.
 DR HSSP; P02023; IBAB.
 DR InterPro; IPR002337; Beta_haem.
 DR IntePro; IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS0103; GLOBIN_1.
 DR METAL; 63 63 IRON (HEME DISTAL LIGAND).
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 FT METAL; 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15958 MW; 57EAB8B694579C93 CRC64;
 DR HBB_SAGNT STANDARD; PRT; 146 AA.
 AC P02037;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 HBB. Hemoglobin beta chain.
 GN Saguinus nigricollis (Black-and-red tamarin), and
 OS *Saguinus oedipus* (Cotton-top tamarin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
 OX NCBI_TAXID=9489, 9490;
 RN [1]
 RP SEQUENCE:
 RC SPECIES=S.nigricollis;
 RX MEDLINE=72020149; PubMed=4999925;
 RA Boyer S.H., Crosby A.N., Noyes A.N., Fuller G.F., Leslie S.E.,
 Donaldson L.J., Vrablik G.R., Schaefer E.W. Jr., Thurmon T.F.;
 RT "Primate hemoglobins: Some sequences and some proposals concerning
 the character of evolution and mutation.";
 RL Blochim. Genet. 5:405-448(1971).
 RN [2]
 RP SEQUENCE:
 RC SPECIES=S.oedipus;
 RX MEDLINE=84212383; PubMed=6427202;
 RA Maita T., Hayashida M., Matsuda G.;
 RT "Primary structures of adult hemoglobins of silvery marmoset,
 Callithrix argenteatus, and cotton-headed tamarin, *Saguinus oedipus*."
 RL Blochim. 95:805-813(1984).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02357; HBMS.
 DR HSSP; P02023; BAB.
 DR InterPro; IPR002337; Beta_haem.
 DR DR Pfam; PR00042; globin; 1.
 DR PRINS; PR00814; BETAHEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 DR PRINTS; PR00814; BETAHEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 DR Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT VARIANT 76 76 A -> T (IN ALLELIC SEQUENCE).
 FT SEQUENCE 146 AA; 15912 MN; 534315F6E3DDC CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 ||||| |||||
 Db 32 LVVYPWTQRF 41

RESULT 99
 HBB_SPAEH ID HBB_SPAEH
 AC P020290;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemeoglobin beta chain.
 HBB OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Spalacinae;
 OC Spalax.
 OX NCBI_TAXID=30637;
 RN [1]
 RP SEQUENCE (KARYOTYPE 2n=60).
 RX MEDLINE=84287390; PubMed=6669215;
 RA Kleinschmidt T., Nevo E., Braunitzer G.;
 RT "The primary structure of the hemoglobin of the mole rat (*Spalax ehrenbergi*, rodentia, chromosome species 60).";
 RT Roppe-Seyler's Z. Physiol. Chem. 365:531-537(1984).
 RN [2]
 RP SEQUENCE (KARYOTYPE 2n=52).
 RX MEDLINE=86000133; PubMed=401241;
 RA Kleinschmidt T., Nevo E., Goodman M., Braunitzer G.;
 RT "Mole rat hemoglobin: primary structure and evolutionary aspects in a
 second karyotype of *Spalax ehrenbergi*, Rodentia, (2n = 52).";
 RT Roppe-Seyler's Z. Physiol. Chem. 366:679-685(1985).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROCTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02406; HBOL.
 DR HSSP; P02067; 1OPW.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PR00042; globin; 1.
 DR PRINTS; PR00814; BETAHEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 DR Heme; Oxygen transport; Transport; Erythrocyte.

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYWPWTFQR 10
 Db 32 LYWPWTFQE 41

RESULT 100

HBB_SPECI HBB_SPECI STANDARD; PRT; 146 AA.

ID HBB_SPECI STANDARD; PRT; 146 AA.

AC P09421; 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.

GN HBB.

OS Spermophilus citellus (European souslik) (Citellus citellus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae; Spermophilus.

OX NCBI_TaxID:9997;

RN [1]

RP SOURCE.

RX MEDLINE:67128535; PubMed=3014354;

RA Soskic V., Grujic-Intar B., Braunitzer G.;

RT "The primary structure of the hemoglobin of the European Souslik (Citellus citellus, Rodentia)."; Biol. Chem. Hoppe-Seyler 367:1159-1166(1986).

RL Chem. Hoppe-Seyler 367:1159-1166(1986).

CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.

CC -!- SUBUNIT: HETEROOTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

PRR: B25359; B23359.

DR HSSP: P02067; 1QBW.

DR InterPro; IPR002337; Beta_haem.

DR InterPro; IPR00071; Globin.

DR pfam; PF00042; globin_1.

DR PRINTS; PR00814; BETAHBEM.

DR PROSITE; PS01033; GLOBIN; 1.

KW Heme; Oxygen transport; Transport; Erythrocyte.

FT METAL 63 63 IRON (HEME DISTAL LIGAND).

FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).

SQ SEQUENCE 146 AA; 15759 MW; 93C40CA2D1418A94 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYWPWTFQR 10
 Db 32 LYWPWTFQE 41

Search completed: July 1, 2002, 12:10:49
 Job time: 217 sec

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L13 ANSWER 1 OF 6 MEDLINE
AN 1999350023 MEDLINE
DN 99350023 PubMed ID: 10423160
TI Antirheumatic agents and leukocyte recruitment. New light on the mechanism
of action of oxaceprol.
AU Parnham M J
CS Pharmacological Institute for the Life Sciences, J.W. Goethe University,
Frankfurt am Main, Germany.. michael.parnham@pliva.hr
SO BIOCHEMICAL PHARMACOLOGY, (1999 Jul 15) 58 (2) 209-15. Ref: 61
Journal code: 9Z4; 0101032. ISSN: 0006-2952.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199908
ED Entered STN: 19990816
Last Updated on STN: 19990816
Entered Medline: 19990805
AB Most anti-inflammatory agents used in the treatment of joint diseases exert inhibitory effects on leukocyte infiltration. Methotrexate, a disease-modifying drug, and corticosteroids also inhibit leukocyte accumulation during inflammation. However, the mechanisms of action of these different compounds on leukocytes vary and in the case of non-steroidal anti-inflammatory drugs (NSAIDs) the mechanism(s) may be indirect. No current drug for inflammatory or degenerative joint disease has been proposed to act specifically by an inhibitory action on neutrophilic leukocytes. Oxaceprol is an amino acid derivative that has been used for several years for the treatment of osteoarthritis and rheumatoid arthritis, ameliorating pain and stiffness and showing good gastrointestinal safety, particularly in comparison with NSAIDs. Recent experimental studies have shown that oxaceprol does not inhibit the synthesis of prostaglandins in vitro, but markedly inhibits neutrophil infiltration into the joints of rats with adjuvant arthritis. These results support earlier screening data showing inhibition by oxaceprol of leukocyte infiltration into sites of acute inflammation. In studies on surgical ischemia reperfusion in hamsters in vivo, oxaceprol was an effective inhibitor of leukocyte adhesion and extravasation. It is proposed that oxaceprol represents a therapeutic agent for degenerative and inflammatory joint diseases, which acts predominantly by inhibiting leukocyte adhesion and migration.

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L2 ANSWER 1 OF 1 MEDLINE
AN 96062323 MEDLINE
DN 96062323 PubMed ID: 7594507
TI An important role for the chemokine
macrophage inflammatory protein-1 alpha in the pathogenesis of the
T cell-mediated autoimmune disease, experimental autoimmune
encephalomyelitis.
AU Karpus W J; Lukacs N W; McRae B L; Strieter R M; Kunkel S L; Miller S D
CS Department of Microbiology and Immunology, Northwestern University
Medical
School, Chicago, IL 60611, USA.
NC AI35934 (NIAID)
HL50057 (NHLBI)
NS34510 (NINDS)
+
SO JOURNAL OF IMMUNOLOGY, (1995 Nov 15) 155 (10) 5003-10.
Journal code: IFB; 2985117R. ISSN: 0022-1767.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Abridged Index Medicus Journals; Priority Journals
EM 199512
ED Entered STN: 19960124
Last Updated on STN: 20000303
Entered Medline: 19951218
AB Experimental autoimmune encephalomyelitis (EAE) is a CD4+ T
cell-mediated,
inflammatory demyelinating disease of the central nervous system (CNS)
that serves as a model for the human demyelinating disease, multiple
sclerosis. A critical event in the pathogenesis of EAE is the entry of
both Ag-specific T lymphocytes and Ag-nonspecific mononuclear cells into
the CNS. In the present report we investigated the role of two C-C
chemokines (macrophage inflammatory protein-1 alpha (MIP-1 alpha) and
monocyte chemotactic protein-1) and a C-x-C chemokine (MIP-2) in the
pathogenesis of EAE. Production in the CNS of MIP-1 alpha, but not that
of
MIP-2, a rodent homologue of IL-8, or monocyte chemotactic protein-1,
correlated with development of severe clinical disease. Administration of
anti-MIP-1 alpha, but not that of anti-monocyte chemotactic protein-1,
prevented the development of both acute and relapsing paralytic disease
as
well as infiltration of mononuclear cells into the CNS initiated by the
transfer of neuroantigen peptide-activated T cells. Ab therapy could also
be used to ameliorate the severity of ongoing clinical disease.
Anti-MIP-1
alpha did not affect the activation of encephalitogenic T cells as
measured by cytokine secretion, surface marker expression, and ability to
adoptively transfer EAE. These results demonstrate that MIP-1 alpha plays
an important role in directing the chemoattraction of mononuclear
inflammatory cells in the T cell-mediated autoimmune disease, EAE.

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L3 ANSWER 1 OF 1 MEDLINE
AN 93231454 MEDLINE
DN 93231454 PubMed ID: 8472896
TI **Astrocyte expression of mRNA encoding cytokines IP-10 and JE/MCP-1 in experimental autoimmune encephalomyelitis.**
AU Ransohoff R M; Hamilton T A; Tani M; Stoler M H; Shick H E; Major J A; Estes M L; Thomas D M; Tuohy V K
CS Research Institute, Cleveland Clinic Foundation, Ohio 44195.
NC HL29582 (NHLBI)
NS 29095 (NINDS)
NSK08-01265 (NINDS)
+
SO FASEB JOURNAL, (1993 Apr 1) 7 (6) 592-600.
Journal code: FAS; 8804484. ISSN: 0892-6638.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199305
ED Entered STN: 19930604
Last Updated on STN: 20000303
Entered Medline: 19930518
AB Mononuclear leukocytes preferentially accumulate in the central nervous system (CNS) during the course of experimental autoimmune encephalomyelitis (EAE). To address factors that govern leukocyte trafficking in EAE, we monitored expression of mRNAs encoding IP-10 and JE/MCP-1, which are members of a family of chemoattractant cytokines. A transient burst of IP-10 and JE/MCP-1 mRNA accumulation in the CNS occurred, in close relation to the onset of histologic and clinical disease. In situ hybridizations showed, unexpectedly, that astrocytes were the major source of mRNAs encoding IP-10 and JE/MCP-1. These observations implicate astrocyte-derived cytokines as potential chemoattractants for inflammatory cells during EAE.

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L6 ANSWER 1 OF 1 MEDLINE
AN 95332927 MEDLINE
DN 95332927 PubMed ID: 7608739
TI **Macrophage inflammatory protein-1 alpha in the cerebrospinal fluid of patients with multiple sclerosis and other inflammatory neurological diseases.**
AU Miyagishi R; Kikuchi S; Fukazawa T; Tashiro K
CS Department of Neurology, Hokkaido University School of Medicine, Sapporo, Japan.
SO JOURNAL OF THE NEUROLOGICAL SCIENCES, (1995 Apr) 129 (2) 223-7.
Journal code: JBJ; 0375403. ISSN: 0022-510X.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199508
ED Entered STN: 19950828
Last Updated on STN: 19950828
Entered Medline: 19950815
AB The level of **macrophage inflammatory protein-1 alpha** (MIP-1 alpha), a newly discovered cytokine of chemokine family, was determined in cerebrospinal fluid (CSF) from 18 patients with **multiple sclerosis** (MS) and from control patients with other neurological disorders by an enzyme-linked immunosorbent assay (ELISA). The concentration of MIP-1 alpha in CSF was significantly elevated in MS in relapse (4.4 pg/ml) compared with non-inflammatory neurological disease control samples (0.3 pg/ml) ($p < 0.0002$). These concentrations in MS patients correlated well with leukocyte cell counts and protein content in CSF ($r = 0.845$, $p < 0.0001$; $r = 0.853$, $p < 0.0001$, respectively). In other inflammatory neurological disorders such as Behcet's disease and HTLV-1 associated myelopathy, significantly increased CSF levels of MIP-1 alpha were also observed. Chemokines are reported to play an important role in an early event of inflammation such as lymphocyte traffic. This report is the first study which confirmed the involvement of a chemokine in MS and other inflammatory neurological disorders.

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L2 ANSWER 1 OF 6 MEDLINE
AN 97323420 MEDLINE
DN 97323420 PubMed ID: 9179868
TI Investigation of inhibition angiotensin-converting enzyme (ACE) activity and **opioid** activity of two hemorphins, LVV-hemorphin-5 and VV-hemorphin-5, isolated from a defined peptic hydrolysate of **bovine hemoglobin**.
AU Zhao Q; Piot J M
CS Laboratoire de Genie proteique et cellulaire, Pole Sciences et Technologies, Universite de La Rochelle, France.. qzhao@bio.univ-lr.fr
SO NEUROPEPTIDES, (1997 Apr) 31 (2) 147-53.
Journal code: 8103156. ISSN: 0143-4179.
CY SCOTLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199708
ED Entered STN: 19970902
Last Updated on STN: 19970902
Entered Medline: 19970818
AB Two peptides, LVV-hemorphin-5 and VV-hemorphin-5, were isolated from a defined peptic **bovine hemoglobin** hydrolysate by reversed-phase HPLC. These peptides were identified as 31-38 and 32-38 fragments of **beta chain of bovine hemoglobin**. Their inhibitory activity towards angiotensin-converting enzyme and **opioid** potency were determined. Since their amino acid sequences show close homology with spinorphin, which is found in human cerebrospinal fluid and in the bovine spinal cord, the possible physiological role in vivo of these peptides was discussed.

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L2 ANSWER 2 OF 6 MEDLINE
AN 95319594 MEDLINE
DN 95319594 PubMed ID: 7596489
TI VV-hemorphin-7 and LVV-hemorphin-7 released during in vitro peptic
hemoglobin hydrolysis are morphinomimetic peptides.
AU Garreau I; Zhao Q; Pejoan C; Cupo A; Piot J M
CS Laboratoire de Genie Proteique et Cellulaire, Pole Sciences et
Techniques,
La Rochelle, France.
SO NEUROPEPTIDES, (1995 Apr) 28 (4) 243-50.
Journal code: 8103156. ISSN: 0143-4179.
CY SCOTLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199508
ED Entered STN: 19950817
Last Updated on STN: 20000303
Entered Medline: 19950803
AB Two opioid peptides were generated by in vitro pepsin treatment
of bovine hemoglobin. These peptides were identified
using a GPI test and purified using HPLC chromatographic techniques. They
correspond to fragments 31-40 (LVV-hemorphin-7) and 32-40
(VV-hemorphin-7)
of the beta-chain of bovine
hemoglobin. Binding experiments strongly confirm that
VV-hemorphin-7 and LVV-hemorphin-7 are opioid peptides since
they inhibited [3H]naloxone binding to rat brain membranes. Our results
indicate that VV-hemorphin-7 and LVV-hemorphin-7 exhibit a lesser potency
both in GPI and binding tests. Selectivity and affinity of these purified
peptides and synthetic hemorphin-7 for opioid receptors is
discussed.

2 type?
Neuropeptides 9s

MW
delta opioid antagonist.

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L2 ANSWER 5 OF 6 MEDLINE
AN 93080543 MEDLINE
DN 93080543 PubMed ID: 1449465
TI Isolation and characterization of two **opioid** peptides from a **bovine hemoglobin** peptic hydrolysate.
AU Piot J M; Zhao Q; Guillochon D; Ricart G; Thomas D
CS Laboratoire de Technologie des Substances Naturelles, Villeneuve D'Ascq, France.
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1992 Nov 30) 189
(1) 101-10.
Journal code: 0372516. ISSN: 0006-291X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199212
ED Entered STN: 19930129
Last Updated on STN: 19930129
Entered Medline: 19921230
AB Two **opioid** peptides were isolated from a **bovine hemoglobin** hydrolysate, by use of gel permeation (GP) and reverse phase (RP) high performance liquid chromatography (HPLC). Their primary structure and accurate molecular weights, determined by amino acid analysis and fast atom bombardment (FAB) mass spectrometry, were identical to fragments 31-40 (LVV-hemorphin-7) and 32-40 (VV-hemorphin 7) of the **beta-chain** of **bovine hemoglobin**. The same fragments occur in human hemoglobin in positions 32-41 and 33-41 of the **beta-chain**, respectively. The **opioid** potency of these peptides, exhibited by use of electrically stimulated muscle of isolated guinea-pig ileum (GPI), were significant and comparable with some others previously described. In addition, the location of the two **opioid** peptides, VV-hemorphin-7 and LVV-hemorphin-7, revealed the existence of a "strategic zone" both in the bovine and human **beta-chains** of hemoglobin.

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L2 ANSWER 3 OF 6 MEDLINE
AN 95305417 MEDLINE
DN 95305417 PubMed ID: 7785876
TI Peptic hemoglobin hydrolysis in an ultrafiltration reactor at pilot plant scale generates **opioid** peptides.
AU Zhao Q; Piot J M; Sannier F; Guillochon D
CS Laboratoire de Genie Proteique, Faculte des Sciences de La Rochelle, France.
SO ANNALS OF THE NEW YORK ACADEMY OF SCIENCES, (1995 Mar 31) 750 452-8.
Journal code: 7506858. ISSN: 0077-8923.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199507
ED Entered STN: 19950726
Last Updated on STN: 19950726
Entered Medline: 19950720
AB Two hemorphins, peptides with **opioid** activity, have been isolated from a pepsin hydrolysate of **bovine hemoglobin**, by use of gel permeation (GP) and reverse phase (RP) high-performance liquid chromatography (HPLC). Their primary structure and accurate molecular weights, determined by amino acid analysis and fast atom bombardment (FAB) mass spectrometry, were identical to fragments 31-40 (LVV-hemorphin-7) and 32-40 (VV-hemorphin 7) of the **beta-chain of bovine hemoglobin**. Two other peptides, 34-40 (hemorphin-7) and 34-41 (hemorphin-8) of the **beta-chain of bovine hemoglobin**, have been synthesized and studied. The **opioid** potency of these peptides, exhibited by the use of electrically stimulated muscle of isolated guinea pig ileum (GPI), were significant and comparable with some others previously described. Studies of **opioid** activities and primary structure of hemorphins led us to postulate the important role of arginine and phenylalanine in **opioid** potency.

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L12 ANSWER 5 OF 105 MEDLINE
AN 95341807 MEDLINE
DN 95341807 PubMed ID: 7616689
TI Effects of footshock-, psychological- and forced swimming-stress on the learning and memory processes: involvement of opioidergic pathways.
AU Jodar L; Takahashi M; Kaneto H
CS Department of Pharmacology, Faculty of Pharmaceutical Sciences, Nagasaki University, Japan.
SO JAPANESE JOURNAL OF PHARMACOLOGY, (1995 Feb) 67 (2) 143-7.
Journal code: 2983305R. ISSN: 0021-5198.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199508
ED Entered STN: 19950905
Last Updated on STN: 19950905
Entered Medline: 19950824
AB Modulation of learning and memory acquisition, retention and retrieval in the one trial passive avoidance learning task in mice by three inescapable stresses, i.e., footshock (FS), psychological (PSY) and forced swimming (SW) were investigated. Pre-, post-training and pre-test FS-stress (2 mA, 0.2 Hz, 1 sec for 30 min) and pre-training PSY-stress (communication box, 5 min) resulted in enhanced test latencies. On the contrary, SW-stress (20 degrees C, 5 min) immediately or 1 hr after training impaired retention latencies that tended to recover after 2 hr post-training SW-stress, suggesting that at least 2 hr are required to consolidate newly acquired information. In contrast, pre-stress **naloxone** (Nx), which did not affect FS- and PSY-stress induced facilitatory effects, returned to control levels the impaired retention latencies induced by SW-stress. Taken collectively, these results imply the involvement of an **opioid**-dependent mechanism in the modulation of **memory** by SW-stress and non-**opioid** in the case of FS- and PSY-stress. Furthermore, they suggest that different mechanisms are involved in stress-induced **memory** modifications and the production of stress-induced analgesia (SIA) since in the latter, FS and PSY but not SW stress produce Nx-sensitive antinociception.

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L12 ANSWER 7 OF 105 MEDLINE
AN 95220477 MEDLINE
DN 95220477 PubMed ID: 7705450
TI Relationship between morphine and etonitazene-induced working memory impairment and analgesia.
AU Braida D; Gori E; Sala M
CS Institute of Pharmacology, Faculty of Mathematical, Physical and Natural Sciences, University of Milan, Italy.
SO EUROPEAN JOURNAL OF PHARMACOLOGY, (1994 Dec 27) 271 (2-3)
497-504.
Journal code: 1254354. ISSN: 0014-2999.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199505
ED Entered STN: 19950518
Last Updated on STN: 19950518
Entered Medline: 19950509
AB An 8-arm radial maze task was used to assess the possible role of the opiate system in the spatial memory of the rat. Increasing doses of etonitazene (0.005-0.06 mg/kg i.p.) and morphine (2.5-100 mg/kg i.p.) significantly impaired performance in the working memory components of the task. For both drugs this impairment was linearly related to the log of the administered dose, and the log-dose relationships were parallel. The regression lines calculated for each parameter for both drugs were parallel thus allowing us to calculate the potency: etonitazene proved to about 1000 times more potent than morphine in terms of correct arm entries, the number of errors and the total time taken to complete the task. Moreover, the progressive cognitive impairment produced by both opiates was closely related to an increase in analgesic effect. Pretreatment with naloxone (5 mg/kg i.p.) completely antagonised the disruptive effect of the opiates on working memory. The importance of the mu subtype opiate receptor in cognitive processes is discussed.

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L11 ANSWER 5 OF 215 MEDLINE
AN 96145761 MEDLINE
DN 96145761 PubMed ID: 8593578
TI Brain sites involved in mu-opioid receptor-mediated actions: a 2-deoxyglucose study.
AU Fabian I; Ableitner A
CS Institute of Pharmacology, Toxicology and Pharmacy, Veterinary Faculty, University of Munich, Germany.
SO BRAIN RESEARCH, (1995 Oct 30) 697 (1-2) 205-15.
Journal code: 0045503. ISSN: 0006-8993.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199604
ED Entered STN: 19960422
Last Updated on STN: 20000303
Entered Medline: 19960411
AB Brain regions that may be functionally involved in the neuropharmacological actions of mu-opioid agonists have been examined in conscious rats using the quantitative [¹⁴C]2-deoxyglucose autoradiographic technique. At 0.5 microgram and 1 microgram intracerebroventricularly the highly selective mu-opioid receptor agonist D-Ala₂, MePhe₄, Gly-ol5-enkephalin effected statistically significant increases as well as statistically significant decreases in regional glucose utilization: in limbic structures, such as hippocampal formation, medial amygdala and lateral septum, glucose utilization was most prominently increased after D-Ala₂, MePhe₄, Gly-ol5-enkephalin; glucose utilization was further increased in the lateral habenular nucleus, the hypothalamus, ventromedial nucleus and dorsal raphe; whereas decreases were found in the mamillary body and anterior thalamus. Glucose utilization in structures associated with somatosensory and nociceptive processing was increased in the central gray of the midbrain and decreased in the nucleus gelatinosus. Only increases in glucose utilization were produced by D-Ala₂; MePhe₄, Gly-ol5-enkephalin in brain regions involved in motor control, including the globus pallidus, the substantia nigra, pars reticulata, the nucleus ruber and the cerebellum, and brain regions involved in visual processing--the visual cortex and superior colliculus deep layer. It is concluded that this pattern of regional changes underlies the mu-opioid receptor-mediated antinociceptive-, epileptogenic-, memory- and mood-modulating actions of mu-opioid agonists.

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L12 ANSWER 10 OF 105 MEDLINE
AN 95093656 MEDLINE
DN 95093656 PubMed ID: 8000575
TI **Naloxone** ameliorates the learning deficit induced by pentylenetetrazol kindling in rats.
AU Becker A; Grecksch G; Brosz M
CS Institute of Pharmacology and Toxicology, Faculty of Medicine, Otto-von-Guericke University Magdeburg, Germany.
SO EUROPEAN JOURNAL OF NEUROSCIENCE, (1994 Sep 1) 6 (9) 1512-5.
Journal code: 8918110. ISSN: 0953-816X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199501
ED Entered STN: 19950215
Last Updated on STN: 19950215
Entered Medline: 19950125
AB Endogenous opioid peptides modulate and regulate processes of central excitability. Furthermore, opioids are thought to interfere with processes of learning and memory storage. In order to study the effects of endogenous opioids on both processes we injected in the course of development of pentylenetetrazol kindling the opiate receptor antagonist naloxone, and tested the animals afterwards in a shuttle-box task. It was found that naloxone pretreatment had dissociative effects. There was no effect on seizure outcome, whereas the learning deficit was ameliorated in the kindled group. The data suggest that endogenous opioid peptides contribute to the learning deficit found in pentylenetetrazol-kindled rats.

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L12 ANSWER 1 OF 105 MEDLINE
AN 96155020 MEDLINE
DN 96155020 PubMed ID: 8587905
TI **Memory** retrieval enhancement by kappa **opioid** agonist
and mu, delta antagonists.
AU Ilyutchenok R Y; Dubrovina N I
CS Laboratory of the Memory Mechanisms, Institute of Physiology Siberian
Branch of the Russian Academy of Medical Sciences, Novosibirsk, Russia.
SO PHARMACOLOGY, BIOCHEMISTRY AND BEHAVIOR, (1995 Dec) 52 (4)
683-7.
Journal code: 0367050. ISSN: 0091-3057.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199603
ED Entered STN: 19960404
Last Updated on STN: 19960404
Entered Medline: 19960327
AB The present study sought to identify specific **opioid** receptor
subtypes involved in the modulation of reactivation of amnesic or
forgotten **memory** traces by use of a one-trial inhibitory
avoidance training procedures in mice. The effects of **naloxone**,
ICI 174,864 (mu and delta opioid receptor antagonists, respectively) and
dynorphin (kappa agonist) were investigated. The results indicated that
preretention test administration of **naloxone** (2 mg/kg) or ICI
174,864 (3 mg/kg) attenuated the amnesia and forgetting as indicated by
prolongation of step-through latency. On the other hand, the activation
of
kappa opioid receptors by dynorphin (1 mg/kg) also showed reactivating
effects both after amnesia and forgetting. On the basis of the
parallelism
of the effects for mu and delta opioid receptor antagonists and kappa
agonist, and on the finding that all three **opioids** demonstrated
a different degree of reactivation of amnesic and forgotten **memory**
traces, it was concluded that mu, delta, and kappa **opioid**
receptors contribute to the modulation of amnesia and forgetting by
independent mechanisms.

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L2 ANSWER 3 OF 3 MEDLINE
AN 94311913 MEDLINE
DN 94311913 PubMed ID: 8037741
TI Isolation of endogenous hemorphin-related hemoglobin fragments from bovine brain.
AU Karelina A A; Philippova M M; Karelina E V; Ivanov V T
CS Shemyakin and Ovchinnikov Institute of Bioorganic Chemistry, Russian Academy of Sciences, Moscow.
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1994 Jul 15) 202 (1) 410-5.
Journal code: 0372516. ISSN: 0006-291X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199408
ED Entered STN: 19940825
Last Updated on STN: 19940825
Entered Medline: 19940815
AB Six short-chain peptides were isolated from an acidic extract of bovine brain in the course of total peptide screening. Their primary structures determined by Edman degradation were LVVYP³⁵, LVVYPWT³⁷, LVVYPWTQ³⁸,
³⁴⁰ LVVYPWTQRF³⁹ and VVYPWTQRF⁴⁰, which respectively corresponded to the fragments 31-35, 31-37, 31-38, 31-40, 32-38 and 32-40 of bovine hemoglobin beta-chain. All these peptides contained sequences of opioid peptides - hemorphins. For two of these peptides, viz. 32-38 and 31-40, isolated from other sources, an opioid activity was demonstrated formerly.

opiod activity

in learning memory

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L6 ANSWER 73 OF 89 MEDLINE
AN 89129128 MEDLINE
DN 89129128 PubMed ID: 3222356
TI Behavioral effects of **angiotensin** II and **angiotensin** II-(4-8)-pentapeptide in rats.
AU Braszko J J; WLasienko J; Kupryszeowski G; Witczuk B; Wisniewski K
CS Department of Pharmacology, Medical Academy, Bialystok, Poland.
SO PHYSIOLOGY AND BEHAVIOR, (1988) 44 (3) 327-32.
Journal code: 0151504. ISSN: 0031-9384.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198903
ED Entered STN: 19900308
Last Updated on STN: 19970203
Entered Medline: 19890323
AB One nM of **angiotensin** II (AII) or **angiotensin** II-(4-8)-pentapeptide [AII(4-8)] given intracerebroventricularly did not affect locomotor and exploratory behavior of rats in open field. AII significantly increased and AII(4-8) did not affect vertical activity of animals in electromagnetic motimeter. Neither of the peptides influenced horizontal activity in the motimeter. Both peptides intensified stereotypy produced by apomorphine and amphetamine. AII significantly improved, while AII(4-8) did not affect, consolidation of **memory** of the correct way to food in T-maze. Similarly, AII increased and AII(4-8) did not change the rate of acquisition of conditioned avoidance responses in a shuttle-box. Of the two examined peptides only AII significantly improved retrieval of **memory** of the passive avoidance behavior. The results show that AII(4-8) influences central dopaminergic system but, unlike its parent peptide AII, has no apparent effect on **memory**.

L6 ANSWER 74 OF 89 MEDLINE
AN 88335764 MEDLINE
DN 88335764 PubMed ID: 3420007
TI Effect of **angiotensin** II and saralasin on motor activity and the passive avoidance behavior of rats.
AU Braszko J J; Wisniewski K
CS Department of Pharmacology, Medical Academy, Bialystok, Poland.
SO PEPTIDES, (1988 May-Jun) 9 (3) 475-9.
Journal code: 8008690. ISSN: 0196-9781.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198810
ED Entered STN: 19900308
Last Updated on STN: 19970203
Entered Medline: 19881021
AB One nmole of **angiotensin** II (ANG II) or saralasin, given intracerebroventricularly, failed to alter the motor activity of rats in open field. A combined injection of both peptides caused a significant decrease of the number of crossings and rearings. In the electromagnetic motimeter horizontal activity of animals was changed by neither of the peptides while the vertical activity was increased by ANG II. Again, a combined injection of saralasin and ANG II inhibited both horizontal and vertical activity. Stereotypies evoked by both apomorphine (2 mg/kg) and

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amphetamine (6.5 mg/kg), given intraperitoneally, were markedly intensified by ANG II and saralasin. A five-fold increase of the re-entry latencies in the passive avoidance situation was observed after pre-test administration of ANG II or saralasin but not the two in combination. These results suggest that ANG II and saralasin may improve processes related to **learning** and **memory** through an unspecific mechanism involving central dopamine systems.

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L6 ANSWER 69 OF 89 MEDLINE
AN 89295885 MEDLINE
DN 89295885 PubMed ID: 3252173
TI **Angiotensin II-(3-8)-hexapeptide affects motor activity, performance of passive avoidance and a conditioned avoidance response in rats.**
AU Braszko J J; Kupryszewski G; Witczuk B; Wisniewski K
CS Department of Pharmacology, Medical Academy, Bialystok, Poland.
SO NEUROSCIENCE, (1988 Dec) 27 (3) 777-83.
Journal code: 7605074. ISSN: 0306-4522.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198908
ED Entered STN: 19900309
Last Updated on STN: 19900309
Entered Medline: 19890801
AB **Angiotensin II-(3-8)-hexapeptide**, at the dose of 1 nmol given intracerebroventricularly, only slightly less than **angiotensin II** (the same dose and route) stimulated exploratory locomotor behaviour in an open field and electromagnetic motimeter. Both peptides considerably enhanced stereotyped behaviour produced by apomorphine and amphetamine. **Angiotensin II-(3-8)-hexapeptide** improved recall in a passive avoidance situation as well as **angiotensin II**. The 3-8 C-terminus of **angiotensin II** enhanced acquisition of active avoidance nearly as effectively as the complete peptide. The results indicate that the effectiveness of equimolar doses of **angiotensin II-(3-8)-hexapeptide** and **angiotensin II** in improving processes related to learning and memory in rats is almost identical and thus must be independent of specific **angiotensin** receptors in brain to which the hexapeptide binds with about 1000 times lower affinity than **angiotensin II**. The stimulation of stereotypy, a dopamine-controlled behaviour, by the peptides points to the possibility of dopaminergic mediation of their psychotropic effects.

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L6 ANSWER 51 OF 89 MEDLINE
AN 94036192 MEDLINE
DN 94036192 PubMed ID: 8221142
TI **Angiotensin II(3-8) (ANG IV) hippocampal binding: potential role in the facilitation of memory.**
AU Wright J W; Miller-Wing A V; Shaffer M J; Higginson C; Wright D E; Hanesworth J M; Harding J W
CS Department of Psychology, Washington State University, Pullman 99164-4820.
NC HL-32063 (NHLBI)
SO BRAIN RESEARCH BULLETIN, (1993) 32 (5) 497-502.
Journal code: 7605818. ISSN: 0361-9230.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199312
ED Entered STN: 19940117
Last Updated on STN: 19940117
Entered Medline: 19931207
AB The present research characterizes a newly discovered ANG II(3-8) (ANG IV) binding site localized in structures associated with **memory** function (hippocampus, neocortex, cerebellum), as well as other brain stem structures (thalamus, inferior olfactory nucleus). This site is not the AT1 or AT2 site that binds **angiotensins** II (ANG II) and III (ANG III) nor does it bind the nonpeptide AT1 or AT2 receptor antagonists DuP753 and PD123177, respectively. The intracerebroventricular (ICV) infusion of ANG IV was ineffective at inducing drinking in rats as compared with equivalent doses of ANG II and III. Although not as effective as ANG II or ANG III, ICV infusion of ANG IV did provoke a pressor response at the highest dose (100 pmol/min), which appeared to be mediated by ANG II (AT1)-type receptors and not the specific AIV binding site described here. By contrast, the ICV infusion of ANG IV resulted in greater effects upon retention and retrieval of a passive avoidance task as compared with ANG II. Specifically, ANG II was not different from the ICV infusion of artificial cerebrospinal fluid, while ANG IV improved retention and retrieval of this task.

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L6 ANSWER 43 OF 89 MEDLINE
AN 95400763 MEDLINE
DN 95400763 PubMed ID: 7670888
TI **Angiotensin II and its 3-7 fragment improve recognition but not spatial memory in rats.**
AU Braszko J J; Kulakowska A; Wisniewski K
CS Department of Pharmacology, Bialystok Medical Academy, Poland.
SO BRAIN RESEARCH BULLETIN, (1995) 37 (6) 627-31.
Journal code: 7605818. ISSN: 0361-9230.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199510
ED Entered STN: 19951026
Last Updated on STN: 19951026
Entered Medline: 19951018
AB The effects of **angiotensin II** (AII), its 3-7 fragment {AII(3-7)} and the substituted 3-7 fragment [Leu-5,AII(3-7)] given intracerebroventricularly (ICV) at the dose of 1 nmole each, on spatial **memory** and recognition were tested. AII(3-7) increased while Leu-5,AII(3-7) slightly decreased session to session foot shock reinforced runtime to the goal in a complex 6 chamber maze. The animals treated with AII performed in the maze similarly to saline injected controls. Overall number of errors was unchanged in all peptide treated groups in comparison with the control group. Object recognition was significantly improved in all the peptide treated groups except for the Leu-5,AII(3-7) group. The results point to the facilitation of recognition and lack of influence on, or even attenuation of, spatial **memory** by AII and its 3-7 fragment. Leu-5,AII(3-7) caused similar though less pronounced effects.

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L6 ANSWER 41 OF 89 MEDLINE
AN 96260253 MEDLINE
DN 96260253 PubMed ID: 8787210
TI The contribution of AT1 and AT2 **angiotensin** receptors to its cognitive effects.
AU Braszko J
CS Clinical Pharmacology Unit, Medical Academy of Bialystok, Poland.
SO ACTA NEUROBIOLOGIAE EXPERIMENTALIS, (1996) 56 (1) 49-54.
Journal code: 1246675. ISSN: 0065-1400.
CY Poland
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199609
ED Entered STN: 19961008
Last Updated on STN: 19980206
Entered Medline: 19960923
AB In this study I attempted to assess, in rats, the role of AT1 and AT2 **angiotensin** receptor subtypes in the phenomenon of improved learning and **memory** after an intracerebroventricular (icv) injection of **angiotensin** II (Ang II) and Ang II (3-7). Selective AT1 (losartan, 1 mg) or AT2 (CGP 42112 A, 2 micrograms) receptor antagonist was dissolved in 2 microliters of saline and given to the left cerebral ventricle 5 min before 1 nmol Ang II or Ang II (3-7) injected in the same volume of saline to the right ventricle. Consequently, there were 9 experimental groups which underwent 3 **memory** oriented and 3 auxiliary tests. Ang II and Ang II (3-7) significantly improved retention of the passive avoidance and recognition **memory**. These effects were abolished by losartan or CGP 42112 A. Better, after Ang II and Ang II (3-7), acquisition of conditioned avoidance responses was unchanged by losartan and abolished by CGP 42112 A. None of the treatments significantly changed rats motor behaviour in open field. Losartan as well as CGP 42112 A abolished significant enhancement of apomorphine (1 mg/kg, i.p.) stereotypy caused by Ang II and Ang II (3-7). The results suggest considerable involvement of AT1 and AT2 **angiotensin** receptors in the cognitive enhancement produced by **angiotensins**.

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L6 ANSWER 75 OF 89 MEDLINE
AN 88077383 MEDLINE
DN 88077383 PubMed ID: 3689567
TI Psychotropic effects of **angiotensin** II and III in rats:
locomotor and exploratory vs cognitive behaviour.
AU Braszko J J; Wisniewski K; Kupryszewski G; Witczuk B
CS Department of Pharmacology, Medical Academy, Bialystok, Poland.
SO BEHAVIOURAL BRAIN RESEARCH, (1987 Sep) 25 (3) 195-203.
Journal code: 8004872. ISSN: 0166-4328.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198802
ED Entered STN: 19900305
Last Updated on STN: 19900305
Entered Medline: 19880217
AB One nmol of **angiotensin** II (AII) or **angiotensin** III
(AIII) given intracerebroventricularly (i.c.v.) increased locomotor and
exploratory activity in an open field apparatus but not in the
electromagnetic field motimeter. Both peptides significantly enhanced
stereotyped behaviour produced by apomorphine (2 mg/kg) and amphetamine
(6.5 mg/kg) given intraperitoneally. Also, AII and AIII improved
consolidation but not retrieval of **memory** for an appetitively
reinforced spatial discrimination task in a T-maze. AII as well as AIII,
given prior to the **learning** session on day 1, increased rate of
acquisition of conditioned avoidance responses in a shuttle-box over the
next 7 days. Both **angiotensins**, injected i.c.v. 15 min before
the retention testing, remarkably (5-fold) prolonged re-entry latencies
in
the passive avoidance situation, suggesting facilitation of the retrieval
of **memory** for an aversively motivated behaviour.

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